

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:04:11 ; Search time 37.4865 Seconds  
(without alignments)  
159.920 Million cell updates/sec

Title: US-10-030-485A-6  
Perfect score: 93  
Sequence: 1 ADSNKTTRIDEANQRATKML 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL 25:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriaph:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	93	100.0	124	13	Q93578 brachydanio
2	93	100.0	143	6	Q9GM34 macaca fasc
3	93	100.0	203	13	Q93579 brachydanio
4	79	84.9	206	13	Q8AXM2 xenopus lae
5	79	84.9	206	13	Q8AXM1 xenopus lae
6	75	80.6	214	13	Q7ZVE4 brachydanio
7	71	76.3	212	5	Q8T3S4 loligo peal
8	66	71.0	204	13	Q8JIS7 xenopus lae
9	60	64.5	210	11	Q70377 rattus norv
10	60	64.5	210	11	O09044 mus musculu
11	60	64.5	221	11	Q9D3L3 mus musculu
12	55	59.1	210	11	O035620 mus musculu
13	53	57.0	212	5	O01389 hirudo medi
14	51	54.8	125	5	O96576 leucophaea
15	50	53.8	90	5	O96578 leucophaea
16	50	53.8	191	17	Q8ZY72 pyrobaculum

17	48	51.6	207	5	O62414
18	47	50.5	105	16	Q81KF6
19	47	50.5	105	16	Q812M9
20	47	50.5	220	5	Q869G6
21	46	49.5	2315	5	Q952K3
22	46	49.5	2396	5	Q23081
23	45	48.4	83	2	O85440
24	45	48.4	83	2	O85439
25	45	48.4	83	2	O85431
26	44	47.3	83	2	O85438
27	44	47.3	207	5	Q8IAE1
28	44	47.3	207	5	Q8IAE0
29	44	47.3	212	5	Q9VH76
30	44	47.3	212	5	O44419
31	44	47.3	212	5	O76338
32	44	47.3	269	16	Q984J1
33	44	47.3	401	16	Q9PIU7
34	44	47.3	530	4	Q9BWU6
35	44	47.3	573	4	Q9HBY5
36	44	47.3	776	16	Q89QI8
37	44	47.3	1313	4	Q9HCK7
38	44	47.3	1787	16	Q8Y4Z2
39	44	47.3	2029	4	Q9C014
40	44	47.3	2069	4	Q9C013
41	44	47.3	2073	4	Q9C012
42	44	47.3	2090	4	Q9HAT7
43	44	47.3	2096	4	Q9UH61
44	43.5	46.8	55	4	Q8NCR8
45	43	46.2	353	16	Q8FNU8

ALIGNMENTS

RESULT 1

O93578 ID O93578 PRELIMINARY; PRT; 124 AA.  
AC O93578;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Synaptosome-associated protein 25.1 (Fragment).  
GN SNAP25A OR SNAP.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99057281; PubMed=9843147;  
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,  
RA Larhammar D.;  
RT "Cloning of two loci for synapse protein Snap25 in zebrafish;  
RT comparison of paralogous linkage groups suggests loss of one locus in  
RT the mammalian lineage."  
RL J. Neurosci. Res. 54:563-573 (1998).  
DR EMBL; AF091593; AAC64289.1; -.  
DR ZFIN; ZDB-GENE-980526-468; snap25a.  
DR InterPro; IPR000928; SNAP-25.  
DR InterPro; IPR000727; T\_SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR Pfam; PF05739; SNARE; 1.  
DR SMART; SM00397; t\_SNARE; 1.  
DR PROSITE; PS50192; T\_SNARE; 1.  
FT NON TER 1  
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 93; DB 13; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADSNKTTRIDEANQRATKML 19

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|||||
Db 103 ADSNKTREIDANQATKML 121

RESULT 2
Q9GM34
ID Q9GM34 PRELIMINARY; PRT; 143 AA.
AC Q9GM34;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049852; BAB16738.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
KW Hypothetical protein.
SQ SEQUENCE 143 AA; 16043 MW; D625DBAA0893FE0 CRC64;

Query Match 100.0%; Score 93; DB 6; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTREIDANQATKML 19
Db 122 ADSNKTREIDANQATKML 140

RESULT 3
O93579
ID O93579 PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein
DE 25,2).
GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL J. Neurosci. Res. 0:0-0(1998).
DR EMBL; AF091594; AAC64290.1; -.
DR EMBL; AF091596; AAC73007.1; -.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.

DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match 84.9%; Score 79; DB 13; Length 206;
Best Local Similarity 84.2%; Pred. No. 6.9e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ADSNKTREIDANQATKML 19
Db 185 ADSNKTREIDANQATKML 203

RESULT 5
Q8AXM1
ID Q8AXM1 PRELIMINARY; PRT; 206 AA.
AC Q8AXM1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNAP25b (Hypothetical protein).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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RT of nuclear membrane vesicles."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033718; BAC06591.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 2.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 204 AA; 22771 MW; D034F75E638E8805 CRC64;

Query Match 71.0%; Score 66; DB 13; Length 204;
Best Local Similarity 63.2%; Pred. No. 0.0092;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRTAKML 19
Db 185 AETNKTTRIDEANTKAKKLI 203

RESULT 9
O70377 PRELIMINARY; PRT; 210 AA.
AC O70377;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNAP-23.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162237; PubMed=10051443;
RA St-Denis J.F., Cabaniols J.P., Cushman S.W., Roche P.A.;
RT "SNAP-23 participates in SNARE complex assembly in rat adipose cells."
RL Biochem. J. 338:709-715(1999).
DR EMBL; AF052596; AAC06031.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 2.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 210 AA; 23235 MW; OD63E3A6F9FE3BA2 CRC64;

Query Match 64.5%; Score 60; DB 11; Length 210;
Best Local Similarity 63.2%; Pred. No. 0.091;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRTAKML 19
Db 190 ADTNKNRDIANTKAKKLI 208

RESULT 10
O09044 PRELIMINARY; PRT; 210 AA.
AC O09044;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SYNDET (SNAP-23) (Synaptosomal-associated protein, 23KD).
GN SNAP23 OR SNTD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Fat;
RX MEDLINE=97312558; PubMed=9168999;
RA Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H.,
RA Niki T., Okazawa H., Kubota T., Kasuga M.;
RT "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c."
RL Biochem. Biophys. Res. Commun. 234:257-262(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97220227; PubMed=9067602;
RA Wang G., Witkin J.W., Hao G., Bankaitis V.A., Scherer P.E.,
RA Baldini G.;
RT "SynDET is a novel SNAP-25 related protein expressed in many tissues."
RL J. Cell Sci. 110:505-513(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Vaidyanathan V.V., Roche P.A.;
RT "Structure and chromosomal localization of the mouse SNAP-23 gene."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojchori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyono-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AB000822; BAA20345.1; -.
DR EMBL; U73143; AAB53597.1; -.
DR EMBL; AF213257; AAF23503.1; -.
DR EMBL; AF213251; AAF23503.1; JOINED.
DR EMBL; AF213252; AAF23503.1; JOINED.
DR EMBL; AF213253; AAF23503.1; JOINED.
DR EMBL; AF213254; AAF23503.1; JOINED.
DR EMBL; AF213255; AAF23503.1; JOINED.
DR EMBL; AF213256; AAF23503.1; JOINED.
DR EMBL; AK019162; BAB31577.1; -.
DR PIR; JC5512; JC5512.
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 210 AA; 23261 MW; 6919E127E16BA2C9 CRC64;

Query Match 64.5%; Score 60; DB 11; Length 210;
Best Local Similarity 63.2%; Pred. No. 0.091;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRTAKML 19
Db 190 ADTNKNRDIANTKAKKLI 208
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RESULT 11

Q9D3L3 ID Q9D3L3 PRELIMINARY; PRT; 221 AA.

AC Q9D3L3; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Synaptoosomal-associated protein, 23kD.

GN SNAP23.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK017311; BAB30686.1; -.

DR MGD; MGI:109356; Snap23.

DR InterPro; IPR000928; SNAP-25.

DR InterPro; IPR000727; T\_SNARE.

DR Pfam; PF00835; SNAP-25; 1.

DR Pfam; PF05739; SNARE; 1.

DR SMART; SM00397; t\_SNARE; 2.

DR PROSITE; PSS0192; T\_SNARE; 2.

SQ SEQUENCE 221 AA; 24550 MW; 368862BE7232DEFB CRC64;

Query Match 64.5%; Score 60; DB 11; Length 221;

Best Local Similarity 63.2%; Pred. No. 0.096;

Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQATKML 19

Db 201 ADTNKNRIDIANTRAKLI 219

RESULT 12

O35620 ID O35620 PRELIMINARY; PRT; 210 AA.

AC O35620;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 23kDa synaptoosomal associated protein.

GN SNAP23 OR MSNAP-23.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Olken S.K., Doerre S., Corley R.B.;

RT "SNARE expression in mouse plasma cells.";

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF007169; AAB62932.1; -.

DR MGD; MGI:109356; Snap23.

DR InterPro; IPR000928; SNAP-25.

DR InterPro; IPR000727; T\_SNARE.

DR Pfam; PF00835; SNAP-25; 1.

DR Pfam; PF05739; SNARE; 1.

DR SMART; SM00397; t\_SNARE; 2.

DR PROSITE; PSS0192; T\_SNARE; 2.

SQ SEQUENCE 210 AA; 23277 MW; FB752FB58D5AE6D9 CRC64;

Query Match 59.1%; Score 55; DB 11; Length 210;

Best Local Similarity 57.9%; Pred. No. 0.6;

Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQATKML 19

Db 190 ADTNKNRIDIANTRPKLI 208

RESULT 13

O01389 ID O01389 PRELIMINARY; PRT; 212 AA.

AC O01389;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE SNAP-25 homolog.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI\_TaxID=6421;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Nerve cord;

RX MEDLINE=97197869; PubMed=9045719;

RA Bruns D., Engers S., Yang C., Ossig R., Jeromin A., Jahn R.;

RT "Inhibition of transmitter release correlates with the proteolytic

RT activity of tetanus toxin and botulinus toxin A in individual cultured

RT synapses of Hirudo medicinalis.";

RL J. Neurosci. 17:1898-1910(1997).

DR EMBL; U85806; AAC47499.1; -.

DR InterPro; IPR000928; SNAP-25.

DR InterPro; IPR000727; T\_SNARE.

DR Pfam; PF00835; SNAP-25; 1.

DR Pfam; PF05739; SNARE; 1.

DR SMART; SM00397; t\_SNARE; 2.

DR PROSITE; PSS0192; T\_SNARE; 2.

SQ SEQUENCE 212 AA; 23802 MW; 8FF591DF32A4FCB6 CRC64;

Query Match 57.0%; Score 53; DB 5; Length 212;

Best Local Similarity 58.8%; Pred. No. 1.3;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 SNKTIDEANQATKML 19

Db 194 SNQLRISDANKRASKLI 210

RESULT 14

O96576 ID O96576 PRELIMINARY; PRT; 125 AA.

AC O96576;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Synaptoosome-associated protein SNAP-25-3 (Fragment).

GN SNAP-3.

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

OC Blaberidae; Leucophaea.

OX NCBI\_TaxID=6988;

RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=99259578; PubMed=10327594;  
RX Johard H.A., Risinger C., Nassel D.R., Larhammar D.;  
RA "The highly conserved synapse protein SNAP-25 displays sequence  
RT variability in the cockroach Leucophaea maderae.";  
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68 (1999).  
DR EMBL; AF091600; AAC69876.1; -.  
DR InterPro; IPR000928; SNAP-25.  
DR InterPro; IPR000727; T\_SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR Pfam; PF05739; SNARE; 1.  
DR SMART; SM00397; t\_SNARE; 1.  
DR PROSITE; PS50192; T\_SNARE; 1.  
FT NON\_TER 1\_1  
SQ SEQUENCE 125 AA; 13985 MW; 72B032879858C316 CRC64;  
  
Query Match 54.8%; Score 51; DB 5; Length 125;  
Best Local Similarity 52.6%; Pred. No. 1.5;  
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 ADSNKTFRIDEANORATKML 19  
Db :||:|||||: :  
105 AESNEERIKVANORASNL 123  
  
RESULT 15  
O96578 PRELIMINARY; PRT; 90 AA.  
AC O96578;  
DT 01-MAY-1999 (TREMELrel. 10, Created)  
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Synaptosome-associated protein SNAP-25-5 (Fragment).  
GN SNAP-5.  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=99259578; PubMed=10327594;  
RX Johard H.A., Risinger C., Nassel D.R., Larhammar D.;  
RA "The highly conserved synapse protein SNAP-25 displays sequence  
RT variability in the cockroach Leucophaea maderae.";  
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68 (1999).  
DR EMBL; AF091602; AAC69878.1; -.  
DR InterPro; IPR000928; SNAP-25.  
DR InterPro; IPR000727; T\_SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR Pfam; PF05739; SNARE; 1.  
DR SMART; SM00397; t\_SNARE; 1.  
DR PROSITE; PS50192; T\_SNARE; 1.  
FT NON\_TER 1\_1  
SQ SEQUENCE 90 AA; 10136 MW; E502D8954676E9F7 CRC64;  
  
Query Match 53.8%; Score 50; DB 5; Length 90;  
Best Local Similarity 57.9%; Pred. No. 1.6;  
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 ADSNKTFRIDEANORATKML 19  
Db :||:|||||: :  
71 AESNEERIKVANORAHNLL 89

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2004, 10:58:06 ; Search time 10.7838 Seconds  
(without alignments)  
91.743 Million cell updates/sec

Title: US-10-030-485A-6  
Perfect score: 93  
Sequence: 1 ADSNKTRIDEANQRATKML 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	93	100.0	203	1 SN2B_CARAU	P36978 carassius a
2	93	100.0	204	1 SN2A_CARAU	P36977 carassius a
3	93	100.0	206	1 SN25_HUMAN	P13795 homo sapien
4	70	75.3	210	1 SN25_TORMA	P36976 torpedo mar
5	56	60.2	211	1 SN23_HUMAN	O00161 homo sapien
6	47	50.5	212	1 SN25_DROME	P36975 drosophila
7	42	45.2	83	1 MULI_PSEAE	P11221 pseudomonas
8	42	45.2	420	1 YEO9_YEAST	P40038 saccharomyc
9	41.5	44.6	181	1 ARF2_MOUSE	P16500 mus musculu
10	41	44.1	494	1 PR31_YEAST	P49704 saccharomyc
11	40	43.0	252	1 YC87_STAEP	Q8CSB6 staphylococ
12	40	43.0	975	1 KINH_DROME	P17210 drosophila
13	39.5	42.5	181	1 ARF1_DICDI	O00909 dictyosteli
14	39	41.9	294	1 CAL2_PARTE	Q94715 paramecium
15	39	41.9	313	1 MRAW_SHEVI	Q9FIN8 shewanella
16	39	41.9	438	1 IAP1_DROME	Q24306 drosophila
17	39	41.9	480	1 ORP2_HUMAN	Q9HIP3 homo sapien
18	39	41.9	970	1 K852_HUMAN	Q9Y6X9 homo sapien
19	38.5	41.4	200	1 SWRI_SERLI	P52989 serratia li
20	38.5	41.4	918	1 YWJB_CABEL	P34487 caenorhabdi
21	38.5	41.4	1337	1 DEXT_STRDO	P39653 streptococc
22	38	40.9	151	1 SYB2_RHIME	Q9Z3Q1 rhizobium m
23	38	40.9	204	1 IPP2_RAT	P50411 rattus norv
24	38	40.9	244	1 1431_ECHGR	Q9U408 echinococcu
25	38	40.9	244	1 1431_ECHMU	Q24902 echinococcu
26	38	40.9	251	1 SN29_ARATH	Q9SD96 arabidopsis
27	38	40.9	263	1 SN30_ARATH	Q9LMS8 arabidopsis
28	38	40.9	385	1 MTLD_LACPL	Q88ZB1 lactobacill
29	38	40.9	473	1 GATB_MYCPU	Q88R09 mycoplasma
30	38	40.9	476	1 ANGT_SHEEP	P20757 ovis aries
31	38	40.9	558	1 YBAL_ECOLI	P39830 escherichia
32	38	40.9	586	1 YEJM_ECOLI	P33922 escherichia
33	38	40.9	675	1 HS7M_PEA	P37900 pisum sativ

34	38	40.9	675	1 UVRB_NEIMA	P56996 neisseria m
35	38	40.9	675	1 UVRB_NEIMB	O33395 neisseria m
36	38	40.9	693	1 SYGB_BACHD	Q9Kd48 bacillus ha
37	38	40.9	1966	1 MYSB_CABEL	P02566 caenorhabdi
38	37.5	40.3	403	1 CID_DROYA	O77027 drosophila
39	37.5	40.3	1397	1 CID_DROME	P19538 drosophila
40	37	39.8	241	1 RRP_HRSV	P14156 human respi
41	37	39.8	241	1 RRP_HRSVA	P03421 human respi
42	37	39.8	241	1 RRP_HRSVL	P12579 human respi
43	37	39.8	266	1 PR11_YEAST	Q07350 saccharomyc
44	37	39.8	329	1 YES7_MYCPN	P75326 mycoplasma
45	37	39.8	372	1 YQIG_BACSU	P54524 bacillus su

ALIGNMENTS

RESULT 1  
SN2B\_CARAU STANDARD; PRT; 203 AA.  
AC P36978;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Synaptosomal-associated protein 25B (SNAP-25B).  
GN SNAP-B.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retina;  
RX MEDLINE=94068448; PubMed=8248151;  
RA Risinger C., Iarhammar D.;  
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).  
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.  
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.  
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.  
CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL; L22976; AAA16538.1; -.  
CC PIR; I50481; I50481.  
CC InterPro; IPR000928; SNAP-25.  
CC InterPro; IPR000727; T\_SNARE.  
CC Pfam; PF00835; SNAP-25; 1.  
CC Pfam; PF05739; SNARE; 1.  
CC SMART; SM00397; t\_SNARE; 2.  
CC PROSITE; PS50192; T\_SNARE; 2.  
CC Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.  
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOLOGY 1.  
FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOLOGY 2.  
FT DOMAIN 85 92 CYS-RICH.  
FT CARBOHYD 77 77 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 185 185 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 203 AA; 22664 MW; 8DFBEBDEB37D6D7 CRC64;

Query Match 100.0%; Score 93; DB 1; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANORATKML 19  
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 Db 182 ADSNKTTRIDEANORATKML 200

## RESULT 2

SN2A CARAU STANDARD; PRT; 204 AA.  
 AC P36977;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Synaptosomal-associated protein 25A (SNAP-25A).  
 GN SNAP-A.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=94068448; PubMed=8248151;  
 RA Risinger C., Larhammar D.;  
 RT "Multiple loci for synapse protein SNAP-25 in the tetraploid  
 RT goldfish."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).  
 CC -!- FUNCTION: May play an important role in the synaptic function of  
 CC specific neuronal systems. Associates with proteins involved in  
 CC vesicle docking and membrane fusion.  
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of  
 CC the nerve terminal.  
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; L22973; AAA16537.1; -  
 PIR; I50480; I50480.  
 DR InterPro; IPR000928; SNAP-25.  
 DR InterPro; IPR000727; T-SNARE.  
 DR Pfam; PF00835; SNAP-25; 1.  
 DR Pfam; PF05739; SNARE; 1.  
 DR SMART; SM00397; t-SNARE; 2.  
 DR PROSITE; PS50192; T-SNARE; 2.  
 KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.  
 FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.  
 FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOMOLOGY 2.  
 FT DOMAIN 85 92 CYS-RICH.  
 SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;

Query Match 100.0%; Score 93; DB 1; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANORATKML 19  
 |||||  
 Db 183 ADSNKTTRIDEANORATKML 201

## RESULT 3

SN25\_HUMAN

SN25\_HUMAN STANDARD; PRT; 206 AA.  
 AC P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).  
 GN SNAP25 OR SNAP.  
 OS Homo sapiens (Human).  
 OS Macaca mulatta (Rhesus macaque).  
 OS Mus musculus (Mouse).  
 OS Rattus norvegicus (Rat).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606; 9544; 10090; 10116; 9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
 RC SPECIES=Human; TISSUE=Brain;  
 RX MEDLINE=94156217; PubMed=8112622;  
 RA Bark I.C., Wilson M.C.;  
 RT "Human cDNA clones encoding two different isoforms of the nerve  
 RT terminal protein SNAP-25."  
 RL Gene 139:291-292(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).  
 RC SPECIES=Human; TISSUE=Brain;  
 RX MEDLINE=94333829; PubMed=8056350;  
 RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;  
 RT "Cloning and sequence analysis of the human SNAP25 cDNA."  
 RL Gene 145:313-314(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC SPECIES=Human; TISSUE=Skeletal muscle;  
 RX MEDLINE=96332494; PubMed=8760387;  
 RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,  
 RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,  
 RA Frenkel M.J., Ward C.W.;  
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25  
 RT (synaptosomal-associated protein 25) A and B isoforms in addition to  
 RT syntaxin 4 and synaptobrevins 1 and 2."  
 RL Biochem. J. 317:945-954(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human;  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chappman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leheslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20."  
 RL Nature 414:865-871(2001).  
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Human; TISSUE=Eye;  
RX MEDLINE=22389257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[6]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Mouse; STRAIN=BALB/c;  
RX MEDLINE=90078337; PubMed=2592413;  
RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,  
RA Bloom F.E., Wilson M.C.;  
RT "The identification of a novel synaptosomal-associated protein,  
SNAP-25, differentially expressed by neuronal subpopulations.";  
RL J. Cell Biol. 109:3039-3052(1989).  
[8]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Mouse; STRAIN=ILS, and ISS;  
RX MEDLINE=21363810; PubMed=11471062;  
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,  
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;  
RT "High-throughput sequence identification of gene coding variants  
within alcohol-related QTLs.";  
RL Mamm. Genome 12:657-663(2001).  
[9]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).  
RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[10]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;  
RA Strausberg R.L.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
[11]  
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
RC SPECIES=Cat;  
RA Kataoka M.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
[12]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Cat; TISSUE=Brain;  
RA Cho A.R., You K.H.;  
RT "Cloning of the SNAP-25 gene from a rat brain cDNA library.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[13]  
RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).  
RC SPECIES=Cat; TISSUE=Brain;  
RX MEDLINE=99155074; PubMed=10037470;  
RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;  
RT "SNARE complex proteins, including the cognate pair VAMP-2 and  
syntaxin-4, are expressed in cultured oligodendrocytes.";  
RL J. Neurochem. 72:988-998(1999).  
[14]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Chicken; TISSUE=Retina;  
RX MEDLINE=91126080; PubMed=1992470;  
RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,  
RA Wilson M.C.;  
RT "Expression of a conserved cell-type-specific protein in nerve  
terminals coincides with synaptogenesis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).  
[15]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC SPECIES=Chicken;  
RX MEDLINE=93389738; PubMed=8377193;  
RA Bark I.C.;  
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon  
encoding distinct isoforms of the protein.";  
RL J. Mol. Biol. 233:67-76(1993).  
[16]  
RP PALMITOYLATION.  
RC SPECIES=Cat;  
RX MEDLINE=93100552; PubMed=1281490;  
RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;  
RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major  
methionine-rich polypeptide in rapid axonal transport and a major  
Query Match 100.0%; Score 93; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADSNKRTRIDEANQRATKML 19  
DB 185 ADSNKRTRIDEANQRATKML 203  
RESULT 4  
SN25-TORMA STANDARD; PRT; 210 AA.  
ID SN25-TORMA STANDARD; PRT; 210 AA.  
AC P36976;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Synaptosomal-associated protein 25 (SNAP-25).  
OS Torpedo marmorata (Marbled electric ray).



```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hynosaquala; Pristiorajae; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7788;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94043281; PubMed=8226991;
RX Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
RL J. Biol. Chem. 268:24408-24414(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC
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CC
CC EMBL; L22020; AAA49284.1; --
CC PIR; I50552;
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC Pfam; PF00835; SNAP-25; 1.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS50192; T-SNARE; 2.
CC Synaptosome; Neurone; Repeat; Coiled coil.
KW FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 88 96 CYS-RICH.
FT SEQUENCE 210 AA; 23652 MW; 58FE471A9234B8B1 CRC64;
SQ
Query Match 75.3%; Score 70; DB 1; Length 210;
Best Local Similarity 77.8%; Pred. No. 0.00019;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DSNKTRIDEANORATKWL 19
Db 193 DMNKARIDEANKHATKWL 210

RESULT 5
SN23_HUMAN
ID SN23_HUMAN STANDARD; PRT; 211 AA.
AC O00161; O00162; Q13602;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 23 (SNAP-23) (Vesicle-membrane fusion
DE protein SNAP-23).
GN SNAP23.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
RC TISSUE=B-cell;
RX MEDLINE=96278745; PubMed=8663154;
RA Ravichandran V., Chawla A., Roche P.A.;
RT "Identification of a novel syntaxin- and synaptobrevin/VAMP-binding
RT protein, SNAP-23, expressed in non-neuronal tissues.";

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RL J. Biol. Chem. 271:13300-13303(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-23A AND SNAP-23B).
RC TISSUE=Neutrophils;
RX MEDLINE=97224437; PubMed=9070898;
RA Mollinedo F., Lazo P.A.;
RT "Identification of two isoforms of the vesicle-membrane fusion protein
RT SNAP-23 in human neutrophils and HL-60 cells.";
RL Biochem. Biophys. Res. Commun. 231:808-812(1997).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Nadal M., Area E., Mollinedo F., Estivill X., Lazo P.A.;
RT "Exon organization and chromosomal localization of human synaptosomal
RT associated protein-23 (SNAP-23) gene and generation of isoforms by
RT alternative splicing.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
RC TISSUE=Cervix, Placenta, and Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raba S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Jones S.J.M., Marra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: ESSENTIAL COMPONENT OF THE HIGH AFFINITY RECEPTOR FOR
CC THE GENERAL MEMBRANE FUSION MACHINERY AND AN IMPORTANT REGULATOR
CC OF TRANSPORT VESICLE DOCKING AND FUSION.
CC -!- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS AND
CC SYNAPTOBREVINS/VAMPS.
CC -!- SUBCELLULAR LOCATION: MAINLY LOCALIZED TO THE PLASMA MEMBRANE.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=SNAP-23a;
CC IsoId=O00161-1; Sequence=Displayed;
CC Name=SNAP-23b;
CC IsoId=O00161-2; Sequence=VSP 006187, VSP 006188;
CC -!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS WHERE FOUND IN
CC PLACENTA.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC
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CC
CC EMBL; U55936; AAC50537.1; --
CC EMBL; Y09567; CAA70760.1; --
CC EMBL; Y09568; CAA70761.1; --
CC EMBL; AJ011915; CAA09864.1; --
CC EMBL; BC000148; AAH00148.1; --
CC EMBL; BC003686; AAH03686.1; --
CC EMBL; BC022890; AAH22890.1; --
CC PIR; JC5296; JC5296.

```





RA Hannaert V., Hubert J.-C.;  
RT "Cloning and analysis of the gene for the major outer membrane  
RT lipoprotein from *Pseudomonas aeruginosa*.";  
RL Mol. Microbiol. 3:421-428(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89327122; PubMed=2502533;  
RA Duchene M., Barron C., Schweizer A., von Sprecht B.-U., Domdey H.;  
RT "Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular  
RT cloning, sequence, and expression in *Escherichia coli*.";  
RL J. Bacteriol. 171:4130-4137(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=ATCC 15692 / PAO1;  
RX MEDLINE=92268853; PubMed=1588307;  
RA Saint-Onge A., Romeyer F., Lebel P., Masson L., Brousseau R.;  
RT "Specificity of the *Pseudomonas aeruginosa* PAO1 lipoprotein I gene as  
RT a DNA probe and PCR target region within the *Pseudomonadaceae*.";  
RL J. Gen. Microbiol. 138:733-741(1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX STRAIN=ATCC 15692 / PAO1;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an  
RT opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid  
CC anchor.  
CC  
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CC  
CC EMBL; X13748; CAA32013.1; -.  
DR EMBL; M25761; AAA25880.1; -.  
DR EMBL; X58714; CAA41550.1; -.  
DR EMBL; A07695; CAA00707.1; -.  
DR EMBL; AE004712; AAG06241.1; -.  
DR PIR; A33854; A33854.  
DR InterPro; IPR000437; Prok lipoprot S.  
DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.  
KW Outer membrane; Lipoprotein; Signal; Complete proteome; Palmitate.  
FT SIGNAL 1 19  
FT CHAIN 20 83 MAJOR OUTER MEMBRANE LIPOPROTEIN.  
FT LIPID 20 20 N-palmitoyl cysteine.  
FT LIPID 20 20 S-diacylglycerol cysteine.  
SQ SEQUENCE 83 AA; 8835 MW; E87F52B86B04DBA4 CRC64;  
Query Match 45.2%; Score 42; DB 1; Length 83;  
Best Local Similarity 72.7%; Pred. No. 3.1;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 9 DEANORATKML 19  
Db 67 DEANERLRML 77  
RESULT 8  
YE09 YEAST  
ID YE09 YEAST STANDARD; PRT; 420 AA.  
AC P40038;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical 47.0 kDa protein in PF117-CEM1 intergenic region.  
GN YER059W.  
OS Saccharomycetes cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=S288c / AB972;  
RX MEDLINE=97313264; PubMed=9169868;  
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,  
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,  
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,  
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,  
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,  
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,  
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;  
RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V";  
RL Nature 387:78-81(1997).  
CC -!- SIMILARITY: TO YEAST YIL050W.  
CC  
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CC  
CC EMBL; U18813; AAB64595.1; -.  
DR PIR; S50562; S50562.  
DR Germonline; 139139; -.  
DR SGD; S0000861; PCL6.  
DR GO; GO:0005979; P:regulation of glycogen biosynthesis; IGI.  
DR GO; GO:0005981; P:regulation of glycogen catabolism; IGI.  
KW Hypothetical protein.  
SQ SEQUENCE 420 AA; 47007 MW; BD8A0C7A501C94E5 CRC64;  
Query Match 45.2%; Score 42; DB 1; Length 420;  
Best Local Similarity 50.0%; Pred. No. 18;  
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
QY 3 SNKTRIDEANQRATKM 18  
Db 283 SNESLDKANRGADKM 298  
RESULT 9  
ARF2 MOUSE  
ID ARF2 MOUSE STANDARD; PRT; 181 AA.  
AC P16500; P10947;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE ADP-ribosylation factor 2.  
GN ARF2.  
OS Mus musculus (Mouse),  
OS Rattus norvegicus (Rat), and  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090, 10116, 9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX SPECIES=Bovine;  
RX MEDLINE=88289746; PubMed=3135549;  
RA Price S.R., Nightingale M., Tsai S.-C., Williamson K.C., Adamik R.,  
RA Chen H.-C., Moss J., Vaughan M.;  
RT "Guanine nucleotide-binding proteins that enhance choleragen ADP-  
RT ribosyltransferase activity: nucleotide and deduced amino acid  
RT sequence of an ADP-ribosylation factor cDNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:5488-5491(1988).

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[2]
RN SEQUENCE FROM N.A.
RC SPECIES=Bovine; TISSUE=Retina;
RX MEDLINE=93186792; PubMed=8444865;
RA Serventi I.M., Cavanaugh E., Moss J., Vaughan M.;
RT "Characterization of the gene for ADP-ribosylation factor (ARF) 2, a
RT developmentally regulated, selectively expressed member of the ARF
RT family of approximately 20-kDa guanine nucleotide-binding proteins.";
RL J. Biol. Chem. 268:4863-4872(1993).
RN [3]
RN SEQUENCE FROM N.A.
RC SPECIES=Rat; TISSUE=Brain;
RA Nightingale M.S., Price S.R., Tsuchiya M., Moss J., Vaughan M.;
RL Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=97103475; PubMed=8947846;
RA Hosaka M., Toda K., Takatsu H., Torii S., Murakami K., Nakayama K.;
RT "Structure and intracellular localization of mouse ADP-ribosylation
RT factors type 1 to type 6 (ARF1-ARF6).";
RL J. Biochem. 120:813-819(1996).
RN [5]
RN SEQUENCE FROM N.A.
CC -1- FUNCTION: GTP-binding protein that functions as an allosteric
CC activator of the cholera toxin catalytic subunit, an ADP-
CC ribosyltransferase. Involved in protein trafficking; may modulate
CC vesicle budding and uncoating within the Golgi apparatus.
CC -1- SIMILARITY: Belongs to the small GTPase superfamily. Arf family.
-----
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DR EMBL; J03794; AAA30383.1; -
DR EMBL; M88287; AAA30754.1; -
DR EMBL; M88292; AAA18982.1; -
DR EMBL; M88289; AAA18982.1; JOINED.
DR EMBL; M88290; AAA18982.1; JOINED.
DR EMBL; M88291; AAA18982.1; JOINED.
DR EMBL; L12381; AAA40686.1; -
DR EMBL; D87899; BAA13491.1; -
DR PIR; A45422; A45422.
DR PIR; JC4946; JC4946.
DR HSSP; P32889; 1HUR.
DR MGD; MGI:99595; Arf2.
DR InterPro; IPR006688; ARF.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00025; arf; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00177; ARF; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01019; ARF; 1.
KW GTP-binding; Multigene family; Protein transport; Golgi stack.
FT NP_BIND 24 31 GTP (BY SIMILARITY).
FT NP_BIND 67 71 GTP (BY SIMILARITY).
FT NP_BIND 126 129 GTP (BY SIMILARITY).
SQ SEQUENCE 181 AA; 20746 MW; 95BE17A962B83016 CRC64;

Query Match 44.6%; Score 41.5; DB 1; Length 181;
Best Local Similarity 47.4%; Pred. No. 8.8;
Matches 9; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 2 DSN-KTRIDEANQRATKML 19
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DB 93 DSNDRERVNEAREELTQML 111

[2]
RN SEQUENCE FROM N.A.
RC SPECIES=Bovine; TISSUE=Retina;
RX MEDLINE=93186792; PubMed=8444865;
RA Serventi I.M., Cavanaugh E., Moss J., Vaughan M.;
RT "Characterization of the gene for ADP-ribosylation factor (ARF) 2, a
RT developmentally regulated, selectively expressed member of the ARF
RT family of approximately 20-kDa guanine nucleotide-binding proteins.";
RL J. Biol. Chem. 268:4863-4872(1993).
RN [3]
RN SEQUENCE FROM N.A.
RC SPECIES=Rat; TISSUE=Brain;
RA Nightingale M.S., Price S.R., Tsuchiya M., Moss J., Vaughan M.;
RL Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=97103475; PubMed=8947846;
RA Hosaka M., Toda K., Takatsu H., Torii S., Murakami K., Nakayama K.;
RT "Structure and intracellular localization of mouse ADP-ribosylation
RT factors type 1 to type 6 (ARF1-ARF6).";
RL J. Biochem. 120:813-819(1996).
RN [5]
RN SEQUENCE FROM N.A.
CC -1- FUNCTION: GTP-binding protein that functions as an allosteric
CC activator of the cholera toxin catalytic subunit, an ADP-
CC ribosyltransferase. Involved in protein trafficking; may modulate
CC vesicle budding and uncoating within the Golgi apparatus.
CC -1- SIMILARITY: Belongs to the small GTPase superfamily. Arf family.
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DR EMBL; J03794; AAA30383.1; -
DR EMBL; M88287; AAA30754.1; -
DR EMBL; M88292; AAA18982.1; -
DR EMBL; M88289; AAA18982.1; JOINED.
DR EMBL; M88290; AAA18982.1; JOINED.
DR EMBL; M88291; AAA18982.1; JOINED.
DR EMBL; L12381; AAA40686.1; -
DR EMBL; D87899; BAA13491.1; -
DR PIR; A45422; A45422.
DR PIR; JC4946; JC4946.
DR HSSP; P32889; 1HUR.
DR MGD; MGI:99595; Arf2.
DR InterPro; IPR006688; ARF.
DR InterPro; IPR006689; ARF/SAR.
DR InterPro; IPR001806; Ras trnsfrmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00025; arf; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR PRINTS; PR00328; SAR1GTPBP.
DR SMART; SM00177; ARF; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS01019; ARF; 1.
KW GTP-binding; Multigene family; Protein transport; Golgi stack.
FT NP_BIND 24 31 GTP (BY SIMILARITY).
FT NP_BIND 67 71 GTP (BY SIMILARITY).
FT NP_BIND 126 129 GTP (BY SIMILARITY).
SQ SEQUENCE 181 AA; 20746 MW; 95BE17A962B83016 CRC64;

Query Match 44.6%; Score 41.5; DB 1; Length 181;
Best Local Similarity 47.4%; Pred. No. 8.8;
Matches 9; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 2 DSN-KTRIDEANQRATKML 19
||| :|:|:| :|:|
DB 93 DSNDRERVNEAREELTQML 111
```

```
RESULT 10
PR31_YEAST STANDARD; PRT; 494 AA.
AC P49704;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pre-mRNA splicing factor PRP31.
GN PRP31 OR YGR091W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96184869; PubMed=8604353;
RA Weidenhammer E.M., Singh M., Ruiz-Noriega M., Woolford J.L. Jr.;
RT "The PRP31 gene encodes a novel protein required for pre-mRNA
RT splicing in Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 24:1164-1170(1996).
RN [2]
RN SEQUENCE FROM N.A.
RA Wedler H., Scharfe M., Wedler E., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Required for pre-mRNA splicing.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; U31970; AAA74984.1; -
DR EMBL; Z72876; CAA97094.1; -
DR PIR; S64386; S64386.
DR GerOnline; 141403; -.
DR SGD; S0003323; PRP31.
DR GO; GO:0030532; C:small nuclear ribonucleoprotein complex; IDA.
DR GO; GO:0008248; F:pre-mRNA splicing factor activity; IPI.
DR GO; GO:0006371; P:mRNA splicing; IPI.
DR InterPro; IPR002687; Nop.
DR Pfam; PF01798; Nop; 1.
DR ProDom; PD004104; Nop; 1.
KW mRNA processing; mRNA splicing; Nuclear protein.
FT CONFLICT 361 394
FT TNPKRKELGENLGSTRKNSDYRMSDNYKIGWNL ->
FT DQPKKLRAGRKRKYKEKFLSHVRLQNRMEFG (IN
FT REF. 2).
SQ SEQUENCE 494 AA; 55967 MW; 1C320B8630EEF5C8 CRC64;

Query Match 44.1%; Score 41; DB 1; Length 494;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 KTRIDEANQRATKML 19
||| :|:|:| :|:|
DB 442 KHRISEANQQADEF 456

RESULT 11
YC87 STAEF
ID YC87 STAEF STANDARD; PRT; 252 AA.
AC Q8CSB6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0271 protein SE1287.
GN SE1287.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
```

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 12228;
RX  PubMed=12950922;
RA  Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA  Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA  Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT  "Genome-based analysis of virulence genes in a non-biofilm-forming
RL  Staphylococcus epidermidis strain (ATCC 12228).";
RL  Mol. Microbiol. 49:1577-1593(2003).
CC  -|- SIMILARITY: Belongs to the UPF0271 (lamB) family.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AE016748; AA004886.1; -.
DR  HAMAP; MF 00691; -.
DR  InterPro; IPR005501; Lamb_YcsF.
DR  Pfam; PF03746; Lamb_YcsF; 1.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 252 AA; 27709 MW; AL72A4D070E119B7 CRC64;

Query Match 43.0%; Score 40; DB 1; Length 252;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 DSNKTRIDEANORATKML 19
Db 185 DATITNTDEAIQALKMV 202
| : ||| : |||
| : ||| : |||

RESULT 12
KINH DROME
ID KINH DROME STANDARD; PRT; 975 AA.
AC P17210; Q9V7L9;
DT 01-AUG-1990 (Rel. 15, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kinesin heavy chain.
GN KHC OR KIN OR CG7765.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168428; PubMed=2522352;
RA Yang J.T., Laymon R.A., Goldstein L.S.B.;
RT "A three-domain structure of kinesin heavy chain revealed by DNA
RL sequence and microtubule binding analyses.";
RL Cell 56:879-889(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=93030741; PubMed=1384131;
RA Gho M., McDonald K., Ganetzky B., Saxton W.M.;
RT "Effects of kinesin mutations on neuronal functions.";
RL Science 258:313-316(1992).
CC -|- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
CC PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
CC -|- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
CC CHAINS.
CC -|- DOMAIN: Composed of three structural domains: a large globular N-
CC terminal domain which is responsible for the motor activity of
CC kinesin (it hydrolyzes ATP and binds microtubule), a central
CC alpha-helical coiled coil domain that mediates the heavy chain
CC dimerization; and a small globular C-terminal domain which
CC interacts with other proteins (such as the kinesin light chains),
CC vesicles and membranous organelles.
CC -|- MISCELLANEOUS: MUTANT FLIES DISPLAY IMPAIRED ACTION POTENTIAL
CC PROPAGATION AND NEUROTRANSMITTER RELEASE AT NEUROMUSCULAR
CC JUNCTIONS, BUT ARE STILL CAPABLE OF TRANSPORTING CERTAIN
CC MEMBRANES, INCLUDING SYNAPTIC VESICLES, TO THE NERVE TERMINAL.
CC -|- SIMILARITY: Belongs to the kinesin-like protein family. Kinesin
CC subfamily.
CC -----
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CC -----
DR EMBL; M24441; AAA28652.1; -.
DR EMBL; AE003807; AAF58029.1; -.
DR PIR; A31497; A31497.
DR HSSP; P33176; 1BG2.
DR FlyBase; FBgn0001308; Khc.
DR GO; GO:0005871; C:kinesin complex; IDA. IDA.
DR GO; GO:0008017; F:microtubule binding; NAS.
DR GO; GO:0003774; F:motor activity; NAS.
DR GO; GO:0007310; P:ocyte dorsal/ventral axis determination; IMP.
DR GO; GO:0007317; P:regulation of pole plasm oskar mRNA localiz...; IMP.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

```

KW Motor protein; Microtubule; ATP-binding; Coiled coil.  
FT DOMAIN 1 334 KINESIN-MOTOR (BY SIMILARITY).  
FT DOMAIN 335 931 COILED COIL.  
FT DOMAIN 932 975 GLOBULAR.  
FT DOMAIN 180 321 MICROTUBULE-BINDING.  
FT NP BIND 92 99 ATP (BY SIMILARITY).  
FT CONFLICT 515 515 A -> T (IN REF. 1).  
SQ SEQUENCE 975 AA; 110399 MW; 24840EF414790888 CRC64;

Query Match 43.0%; Score 40; DB 1; Length 975;  
Best Local Similarity 42.1%; Pred. No. 1e+02;  
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRATKML 19  
DB 276 ADGNKTHIPYRDSKLTRIL 294

RESULT 13  
ARF1\_DICDI STANDARD; PRT; 181 AA.  
AC O00909;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE ADP-ribosylation factor 1.  
GN ARFA OR ARF1.  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jones D., Morgan C., Insall R., Cockerfoot S.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: GTP-binding protein that functions as an allosteric  
CC activator of the cholera toxin catalytic subunit, an ADP-  
CC ribosyltransferase. Involved in protein trafficking; may modulate  
CC vesicle budding and uncoating within the Golgi apparatus (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Arf family.

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EMBL; AJ000063; CAA03896.1; -.  
HSSP; P32889; 1RRF.  
DictyBase; DB0001681; arfa.  
InterPro; IPR006688; ARF.  
InterPro; IPR006689; ARF/SAR.  
InterPro; IPR001806; Ras trnsfrmng.  
Pfam; PF00025; arf; 1.  
PRINTS; PR00449; RASTRNSFRMNG.  
PRINTS; PR00328; SAR1GTPBP.  
SMART; SM00177; ARF; 1.  
TIGRFAMs; TIGR00231; small\_GTP; 1.  
PROSITE; PS01019; ARF; 1.  
KW GTP-binding; Myristate; Protein transport; Golgi stack; Lipoprotein.  
FT INIT\_MET 0 0 BY SIMILARITY.  
FT LIPID 1 1 N-myristoyl glycine (Potential).  
FT NP\_BIND 23 30 GTP (BY SIMILARITY).  
FT NP\_BIND 66 70 GTP (BY SIMILARITY).  
FT NP\_BIND 125 128 GTP (BY SIMILARITY).  
SQ SEQUENCE 181 AA; 20550 MW; 87AE5F2B2F230158 CRC64;

Query Match 42.5%; Score 39.5; DB 1; Length 181;  
Best Local Similarity 57.9%; Pred. No. 19;  
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 2 DSN-KTRIDEANQRATKML 19  
DB 92 DSNDRERIQAACDELTKML 110

RESULT 14  
CAL2\_PARTE STANDARD; PRT; 294 AA.  
AC Q947I5;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Putative cathepsin L2 (EC 3.4.22.15) (Fragment).  
OS Paramacium tetraurelia.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;  
OC Paramacium.  
OX NCBI\_TaxID=5888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Stock 51;  
RX MEDLINE=96248439; PubMed=8665938;  
RA Voelkel H., Kurz U., Linder J., Klumpp S., Gnau V., Jung G.,  
RA Schultze J.E.;  
RT "Cathepsin L is an intracellular and extracellular protease in  
RT Paramacium tetraurelia: Purification, cloning, sequencing and specific  
RT inhibition by its expressed propeptide";  
RL Eur. J. Biochem. 238:198-206(1996).  
CC -!- FUNCTION: May be involved in extracellular digestion.  
CC -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As  
CC compared to cathepsin B, cathepsin L exhibits higher activity  
CC towards protein substrates, but has little activity on Z-Arg-Arg-  
CC NHMe, and no peptidyl-dipeptidase activity.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to peptidase family C1.  
CC -!- CAUTION: This protein may be non-functional as it lacks the  
CC cysteine active site residue which is replaced by Gly-118.

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EMBL; X91756; CAA62871.1; -.  
PIR; S68784; S68784.  
HSSP; O60911; 1PH0.  
InterPro; IPR000668; Peptidase C1.  
InterPro; IPR000169; SHprot\_acsite.  
Pfam; PF00112; Peptidase\_C1; 1.  
ProDom; PD000158; Peptidase\_C1; 1.  
SMART; SM00645; Pept\_C1; 1.  
PROSITE; PS00640; THIOI\_PROTEASE ASN; FALSE NEG.  
PROSITE; PS00139; THIOI\_PROTEASE\_CYS; FALSE NEG.  
PROSITE; PS00639; THIOI\_PROTEASE\_HIS; FALSE NEG.  
KW Hydrolase; Thiol protease.  
FT NON\_TER 1 1  
FT PROPEP <1 ? ACTIVATION PEPTIDE.  
FT CHAIN ? 294 PUTATIVE CATHEPSIN L2.  
FT SITE 118 118 POSITION OF ACTIVE SITE CYS.  
FT ACT\_SITE 247 247 BY SIMILARITY.  
FT ACT\_SITE 264 264 BY SIMILARITY.  
FT DISULFID 115 156 BY SIMILARITY.  
FT DISULFID 240 284 BY SIMILARITY.  
SQ SEQUENCE 294 AA; 33627 MW; 6FD686A0176BEC51 CRC64;

Query Match 41.9%; Score 39; DB 1; Length 294;  
Best Local Similarity 61.5%; Pred. No. 39;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DSNKTIDEANQR 14



Db 39 NSNKRMEHNR 51

RESULT 15  
MRAW\_SHEVI  
ID MRAW\_SHEVI STANDARD; PRT; 313 AA.  
AC Q9FLN8;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE S-adenosyl-methyltransferase mraw (EC 2.1.1.-).  
GN MRAW.  
OS Shewanella violacea.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
OC Alteromonadaceae; Shewanella.  
OX NCBI\_TaxID=60217;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSS12;  
RA Ishii A., Nakasone K., Sato T., Sugai M., Wachi M., Nagai K., Kato C.;  
RT "Isolation and characterization of dcw gene cluster for cell division  
RT and cell wall synthesis from a deep-sea piezophilic Shewanella  
RT violacea.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase  
CC activity (By similarity).  
CC -!- SIMILARITY: Belongs to the mraw family.  
CC -----  
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CC -----  
DR EMBL; AB052554; BAB19194.1; -.  
DR HAMAP; MF 01007; -; 1.  
DR InterPro; IPR002903; Bac\_Metrnfrase.  
DR Pfam; PF01795; Methyltransf 5; 1.  
DR ProDom; PD004685; Bac\_Metrnfrase; 1.  
DR TIGRFAMs; TIGR00006; TIGR00006; 1.  
KW Transferase; Methyltransferase.  
SQ SEQUENCE 313 AA; 35023 MW; EEF017A946AC43A1 CRC64;  
  
Query Match 41.9%; Score 39; DB 1; Length 313;  
Best Local Similarity 52.9%; Pred. No. 42;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 ADSNKTREIDENQRTK 17  
|:|||||:|:|  
Db 272 AEINKTRLLKAVGKATK 288

Search completed: March 9, 2004, 11:08:10  
Job time : 11.7838 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:07:42 ; Search time 28.2432 Seconds  
(without alignments)  
142.049 Million cell updates/sec

Title: US-10-030-485A-6  
Perfect score: 93  
Sequence: 1 ADSNKTIDEANQRATKML 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PTCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	93	100.0	21	10	US-09-942-024-89
2	93	100.0	21	10	US-09-942-098-89
3	93	100.0	24	10	US-09-942-024-90
4	93	100.0	24	10	US-09-942-098-90
5	93	100.0	33	10	US-09-942-024-33
6	93	100.0	33	10	US-09-942-024-37
7	93	100.0	33	10	US-09-942-024-38
8	93	100.0	33	10	US-09-942-098-33
9	93	100.0	33	10	US-09-942-098-37
10	93	100.0	33	10	US-09-942-098-38
11	93	100.0	116	10	US-09-962-360B-11
12	93	100.0	203	10	US-09-942-024-14
13	93	100.0	203	10	US-09-942-098-14
14	93	100.0	206	10	US-09-942-024-2
15	93	100.0	206	10	US-09-942-024-7

16	93	100.0	206	10	US-09-942-024-12	Sequence 12, Appl
17	93	100.0	206	10	US-09-942-098-2	Sequence 2, Appl
18	93	100.0	206	10	US-09-942-098-7	Sequence 7, Appl
19	93	100.0	206	10	US-09-942-098-12	Sequence 12, Appl
20	89	95.7	18	10	US-09-942-024-32	Sequence 32, Appl
21	89	95.7	18	10	US-09-942-098-32	Sequence 32, Appl
22	89	95.7	23	10	US-09-942-024-88	Sequence 88, Appl
23	89	95.7	23	10	US-09-942-098-88	Sequence 88, Appl
24	87	93.5	116	10	US-09-962-360B-12	Sequence 12, Appl
25	85	91.4	17	10	US-09-942-024-31	Sequence 31, Appl
26	85	91.4	17	10	US-09-942-098-31	Sequence 31, Appl
27	83	89.2	17	10	US-09-942-024-30	Sequence 30, Appl
28	83	89.2	17	10	US-09-942-098-30	Sequence 30, Appl
29	83	89.2	17	13	US-10-011-588-2	Sequence 2, Appl
30	80	86.0	17	10	US-09-942-024-55	Sequence 55, Appl
31	80	86.0	17	10	US-09-942-098-55	Sequence 55, Appl
32	79	84.9	16	10	US-09-942-024-29	Sequence 29, Appl
33	79	84.9	16	10	US-09-942-098-29	Sequence 29, Appl
34	79	84.9	17	10	US-09-942-024-47	Sequence 47, Appl
35	79	84.9	17	10	US-09-942-024-49	Sequence 49, Appl
36	79	84.9	17	10	US-09-942-024-54	Sequence 54, Appl
37	79	84.9	17	10	US-09-942-098-47	Sequence 47, Appl
38	79	84.9	17	10	US-09-942-098-49	Sequence 49, Appl
39	79	84.9	17	10	US-09-942-098-54	Sequence 54, Appl
40	79	84.9	19	10	US-09-942-024-85	Sequence 85, Appl
41	79	84.9	19	10	US-09-942-098-85	Sequence 85, Appl
42	78	83.9	17	10	US-09-942-024-48	Sequence 48, Appl
43	78	83.9	17	10	US-09-942-024-52	Sequence 52, Appl
44	78	83.9	17	10	US-09-942-024-56	Sequence 56, Appl
45	78	83.9	17	10	US-09-942-098-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1  
US-09-942-024-89  
; Sequence 89, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 89  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: 1  
; OTHER INFORMATION: Xaa=fluorescein-modified lysine  
; NAME/KEY: MOD\_RES  
; LOCATION: 21  
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: at the C-terminal  
US-09-942-024-89

Query Match 100.0%; Score 93; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRATKML 19  
|||||

Db 2 ADSNKTTRIDEANQRATKML 20

## RESULT 2

US-09-942-098-89  
; Sequence 89, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; TITLE OF INVENTION: Toxins  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 89  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: 1  
; OTHER INFORMATION: Xaa=fluorescein-modified lysine  
; NAME/KEY: MOD\_RES  
; LOCATION: 21  
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: at the C-terminal  
US-09-942-098-89

Query Match 100.0%; Score 93; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
|||||  
Db 2 ADSNKTTRIDEANQRATKML 20

## RESULT 3

US-09-942-024-90  
; Sequence 90, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 90  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: 1  
; OTHER INFORMATION: Xaa=fluorescein-modified lysine  
; NAME/KEY: MOD\_RES  
; LOCATION: 24  
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(0)

; OTHER INFORMATION: at the C-terminal  
US-09-942-024-90

Query Match 100.0%; Score 93; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.2e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
|||||  
Db 2 ADSNKTTRIDEANQRATKML 20

## RESULT 4

US-09-942-098-90  
; Sequence 90, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; TITLE OF INVENTION: Toxins  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 90  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: 1  
; OTHER INFORMATION: Xaa=fluorescein-modified lysine  
; NAME/KEY: MOD\_RES  
; LOCATION: 24  
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: at the C-terminal  
US-09-942-098-90

Query Match 100.0%; Score 93; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.2e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
|||||  
Db 2 ADSNKTTRIDEANQRATKML 20

## RESULT 5

US-09-942-024-33  
; Sequence 33, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-942-024-33

```
Query Match      100.0%; Score 93; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||||||
Db      12 ADSNKTIDEANQRATKML 30

RESULT 6
US-09-942-024-37
; Sequence 37, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-37

Query Match      100.0%; Score 93; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||||||
Db      12 ADSNKTIDEANQRATKML 30

RESULT 7
US-09-942-024-38
; Sequence 38, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-38

Query Match      100.0%; Score 93; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||||||
Db      12 ADSNKTIDEANQRATKML 30

RESULT 8
US-09-942-098-33
; Sequence 33, Application US/09942098
```

```
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: Toxins
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33

Query Match      100.0%; Score 93; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||||||
Db      12 ADSNKTIDEANQRATKML 30

RESULT 9
US-09-942-098-37
; Sequence 37, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: Toxins
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-37

Query Match      100.0%; Score 93; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||||||
Db      12 ADSNKTIDEANQRATKML 30

RESULT 10
US-09-942-098-38
; Sequence 38, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: Toxins
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
```

; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-098-38

Query Match 100.0%; Score 93; DB 10; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANQATKML 19  
Db 12 ADSNKTIDEANQATKML 30

## RESULT 11

US-09-962-360B-11  
; Sequence 11, Application US/09962360B  
; Publication No. US20030077685A1  
; GENERAL INFORMATION:

; APPLICANT: Schmidt, James J.  
; APPLICANT: Stafford, Robert G.  
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid  
; TITLE OF INVENTION: Neurotoxins  
; FILE REFERENCE: 003/224/SAP  
; CURRENT APPLICATION NUMBER: US/09/962,360B  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/235,050  
; PRIOR FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 11  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1  
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine  
US-09-962-360B-11

Query Match 100.0%; Score 93; DB 10; Length 116;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANQATKML 19  
Db 94 ADSNKTIDEANQATKML 112

## RESULT 12

US-09-942-024-14  
; Sequence 14, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:

; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-024-14

Query Match 100.0%; Score 93; DB 10; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANQATKML 19  
Db 182 ADSNKTIDEANQATKML 200

## RESULT 13

US-09-942-098-14  
; Sequence 14, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; TITLE OF INVENTION: Toxins  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-098-14

Query Match 100.0%; Score 93; DB 10; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANQATKML 19  
Db 182 ADSNKTIDEANQATKML 200

## RESULT 14

US-09-942-024-2  
; Sequence 2, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:

; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-942-024-2

Query Match 100.0%; Score 93; DB 10; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANQATKML 19  
Db 185 ADSNKTIDEANQATKML 203

## RESULT 15

US-09-942-024-7  
; Sequence 7, Application US/09942024  
; Publication No. US20030143650A1

```
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match      100.0%; Score 93; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||||
Db      185 ADSNKTIDEANQRATKML 203
```

Search completed: March 9, 2004, 11:12:07  
Job time : 28.2432 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:04:36 ; Search time 13.8649 Seconds  
(without alignments)  
131.818 Million cell updates/sec

Title: US-10-030-485A-6  
Perfect score: 93  
Sequence: 1 ADSNKTTRIDEANQRTKML 19  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	93	100.0	203	2 I50481	synapse protein SN
2	93	100.0	204	2 I50480	synapse protein SN
3	93	100.0	206	2 A37861	synaptosomal-assoc
4	93	100.0	206	2 I53735	nerve terminal pro
5	93	100.0	206	2 I67823	nerve terminal pro
6	93	100.0	206	2 A33623	synaptosomal-assoc
7	70	75.3	210	2 I50552	synapse protein 23
8	60	64.5	210	2 JC5512	SNARE protein 23
9	56	60.2	158	2 JC5297	vesicle-membrane f
10	56	60.2	211	2 JC5296	vesicle-membrane f
11	48	51.6	234	2 T26553	hypothetical prote
12	46	49.5	2288	2 T29999	synaptosomal-assoc
13	44.5	47.8	29	2 A49708	transmembrane tran
14	44	47.3	401	2 E81436	probable tape-meas
15	44	47.3	1787	2 AG1360	adhesin homolog lm
16	43	46.2	1582	2 AC1153	outer membrane lip
17	42	45.2	83	2 A33854	hypothetical prote
18	42	45.2	219	2 AB1996	hypothetical prote
19	42	45.2	420	2 S50562	hypothetical prote
20	42	45.2	680	2 H70347	outer membrane pro
21	41.5	44.6	181	2 JC4946	ADP-ribosylation f
22	41.5	44.6	181	2 A45422	ADP-ribosylation f
23	41	44.1	201	2 T09047	hypothetical prote
24	41	44.1	393	2 T32127	hypothetical prote
25	41	44.1	438	2 B71963	probable outer mem
26	41	44.1	494	2 S64386	pre-mRNA splicing
27	41	44.1	575	2 F96966	methyl-accepting c
28	41	44.1	642	2 G90551	lipoprotein [impor

30	41	44.1	1578	2 AD1512	peptidoglycan boun
31	40.5	43.5	1314	2 T09481	mating type silenc
32	40	43.0	243	2 T20653	hypothetical prote
33	40	43.0	540	2 T34187	hypothetical prote
34	40	43.0	975	1 A31497	kinesin heavy chai
35	40	43.0	1302	1 JC6009	surface-located me
36	39.5	42.5	180	2 T32978	ADP-ribosylation f
37	39	41.9	71	2 D84748	hypothetical prote
38	39	41.9	294	2 S68784	cathepsin L - Para
39	39	41.9	644	2 D71427	receiver-like prot
40	39	41.9	664	2 T51247	ARR2 protein [impo
41	38.5	41.4	200	2 S71036	swarmer initiation
42	38.5	41.4	918	2 G88545	protein F59B2.12 [
43	38.5	41.4	943	2 S31132	hypothetical prote
44	38.5	41.4	1337	2 T30291	dextranase - Strep
45	38	40.9	105	2 E95039	cell division prot

ALIGNMENTS

RESULT 1  
I50481  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I50481  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MUID:94068448; PMID:8248151  
A:Accession: I50481  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-203 <RIS>  
A:Cross-references: GB:L22976; NID:g349430; PIDN:AAA16538.1; PID:g349431  
C:Genetics:  
A:Gene: SNAP-25

Query Match 100.0%; Score 93; DB 2; Length 203;  
Best Local Similarity 100.0%; Pred. No. 7.6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRTKML 19  
|||||  
Db 182 ADSNKTTRIDEANQRTKML 200  
|||||

RESULT 2  
I50480  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I50480  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MUID:94068448; PMID:8248151  
A:Accession: I50480  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-204 <RIS>  
A:Cross-references: GB:L22973; NID:g349426; PIDN:AAA16537.1; PID:g349427  
C:Genetics:  
A:Gene: SNAP-25

Query Match 100.0%; Score 93; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 7.6e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRTKML 19  
|||||



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Query Match      86.0%; Score 80; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNKTRIDEANQKATKML 19
Db      1 SNKTRIDEANQKATKML 17

RESULT 13
US-08-743-894B-49
; Sequence 49, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-49

Query Match      84.9%; Score 79; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNKTRIDEANQKATKM 18
Db      1 SNKTRIDEANQKATKM 16

RESULT 14
US-08-743-894B-27
; Sequence 27, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
```

```
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
; LOCATION: 13
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-27

Query Match      84.9%; Score 79; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 SNKTRIDEANQKATKML 19
Db      1 SNKTRIDEANQKATKML 17

RESULT 15
US-08-743-894B-30
; Sequence 30, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
```

```

; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 9
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-30

Query Match      84.9%; Score 79; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 SNKTRIDEANQRATKML 19
Db      1 SNKTRIDEXNQRATKML 17

```

Search completed: March 9, 2004, 11:10:59  
Job time : 16.9459 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: March 9, 2004, 10:57:21 ; Search time 52.3784 Seconds  
(without alignments)  
102.493 Million cell updates/sec

Title: US-10-030-485A-6  
Perfect score: 93  
Sequence: 1 ADSNKTRIDEANQRATKML 19  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	19	4	AAB15586 Human SNA
2	93	100.0	21	6	Aae36734 Fret subs
3	93	100.0	24	6	Aae36735 Fret subs
4	93	100.0	26	2	Aaw30099 Neurotran
5	93	100.0	33	6	Aae36682 Goldfish
6	93	100.0	33	6	Aae36683 Goldfish
7	93	100.0	33	6	Aae36678 SNAPE-25 p
8	93	100.0	37	2	Aaw30097 Neurotran
9	93	100.0	70	2	Aar86823 SNAPE-25 r
10	93	100.0	86	4	AAB15584 Human SNA
11	93	100.0	116	5	Aao15165 Clostridi
12	93	100.0	206	2	Aaw30103 Synaptoso
13	93	100.0	206	2	Aaw43426 Mouse syn
14	93	100.0	206	2	Aaw79198 Mouse SNA
15	93	100.0	206	4	Aau00246 Synaptoso
16	93	100.0	206	4	Aau00253 SNAPE hom
17	93	100.0	206	4	Aau00252 SNAPE hom
18	93	100.0	206	6	Aae36662 Human SNA
19	93	100.0	206	6	Aae36667 Rat VAMP-
20	93	100.0	206	7	Ade54280 Rat Prote
21	93	100.0	206	7	Ade54288 Rat Prote
22	93	100.0	206	7	Ade54276 Rat Prote
23	93	100.0	206	7	Ade54290 Human Pro
24	93	100.0	206	7	Ade54282 Rat Prote
25	93	100.0	206	7	Ade54274 Rat Prote

26	93	100.0	206	7	ADE54286 Human Pro
27	93	100.0	206	7	ADE54284 Rat Prote
28	93	100.0	206	7	ADE54272 Rat Prote
29	93	100.0	206	7	ADE54278 Rat Prote
30	89	95.7	18	6	Aae36677 Human SNA
31	89	95.7	23	6	Aae36733 Fret subs
32	89	95.7	206	4	Aau02640 Synaptoso
33	87	93.5	116	5	Aao15166 Clostridi
34	87	93.5	203	4	Aau02636 Synaptoso
35	87	93.5	206	4	Aau00261 Synaptoso
36	87	93.5	206	4	Aau00259 Synaptoso
37	87	93.5	206	4	Aau00260 Synaptoso
38	87	93.5	206	4	Aau02638 Synaptoso
39	86	92.5	206	4	Aau00262 Synaptoso
40	85	91.4	17	6	Aae36676 Human SNA
41	84	90.3	206	4	Aau00266 Synaptoso
42	84	90.3	206	4	Aau00257 Synaptoso
43	83	89.2	17	2	Aay44057 Human SNA
44	83	89.2	17	2	Aay44021 Amino aci
45	83	89.2	17	5	ABG69065 Human pol

ALIGNMENTS

RESULT 1  
AAB15586  
ID AAB15586 standard; peptide; 19 AA.  
XX  
AC AAB15586;  
XX  
DT 02-MAR-2001 (first entry)  
DE Human SNAP-25 N-terminal peptide #6.  
XX  
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;  
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;  
KW neurodegenerative disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200064932-A1.  
XX  
PD 02-NOV-2000.  
PF 18-FEB-2000; 2000WO-ES000058.  
PR 23-APR-1999; 99ES-00000844.  
XX (LIPO-) LIPOTEC SA.  
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;  
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;  
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;  
PI Perez Paya E;  
XX WPI; 2001-007091/01.  
DR  
XX New peptides containing amino acid sequences from known proteins for  
treatment of neurological disorders.  
PT Claim 17; Page 34; 40pp; Spanish.  
XX  
CC The invention relates to new peptides comprising 3-30 contiguous amino  
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated  
CC protein 25). The peptides AAB15581-B15586 represent examples of the  
CC peptides of the invention. The peptides have neuronal exocytosis  
CC inhibitory activity and are used for treatment of facial wrinkles and  
CC asymmetry and pathological neuronal exocytosis-mediated pathological  
CC disorders and alterations manifested e.g. by spasms and neurological and  
XX neurodegenerative disorders  
SQ Sequence 19 AA;

Query Match 100.0%; Score 93; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTTRIDEANQRATKML 19  
| | | | | | | | | | | | | | | | | | |  
Db 1 ADSNKTTRIDEANQRATKML 19

RESULT 2  
AAE36734  
ID AAE36734 standard; peptide; 21 AA.  
XX  
AC AAE36734;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Fret substrate peptide #5 used in the invention.  
XX  
KW Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;  
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;  
KW cosmetic.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is  
FT given as Xaa in the sequence shown as SEQ ID NO: 89 in  
FT the sequence listing of the specification"  
FT  
FT Modified-site 21 /note= "Tetramethylrhodamine-modified Lysine; C-terminal  
FT amide; This residue is given as Xaa in the sequence shown  
FT as SEQ ID NO: 89 in the sequence listing of the  
FT specification"  
XX

WO2003020948-A2.  
XX  
PD 13-MAR-2003.  
XX  
PF 22-AUG-2002; 2002WO-US027145.  
XX  
PR 28-AUG-2001; 2001US-00942024.  
XX  
PA (ALLR ) ALLERGAN INC.  
XX  
PI Steward LE, Fernandez-Salas E, Aoki KR;  
XX  
DR WPI; 2003-290198/28.  
XX  
PS Botulinum serotype A/E substrate useful for assaying protease activity of  
XX botulinum toxins, comprises donor fluorophore, acceptor and a clostridial  
XX toxin recognition sequence that includes a cleavage site.  
XX  
PS Example 1; Page 115; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The  
XX invention further relates to botulinum serotype A/E (BoNT/A/E) substrates  
XX which comprise a donor fluorophore, an acceptor having an absorbance  
XX spectrum overlapping the emission spectrum of the donor fluorophore and a  
XX BoNT A or BoNT/E recognition sequence comprising a cleavage site, where  
XX the cleavage site intervenes between the donor fluorophore and acceptor  
XX and under the appropriate conditions, the resonance energy transfer is  
XX exhibited between the donor and acceptor. Natural targets of clostridium  
XX neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences  
XX of the invention are useful in assaying for the protease activity of any  
XX clostridial toxin including botulinum toxins of all serotypes and tetanus  
XX toxins (TeNT) in a sample including bacterial, baculoviral and yeast  
XX lysate, raw, cooked or processed foods, beverages, animal feed, soil  
XX samples, water samples, cosmetics, tissue samples and beverage or food  
XX samples. They are useful to assay a sample from a human or animal, for  
XX e.g., exposed to clostridial toxin or having one or more symptoms of a

CC clostridial toxin, to follow activity during production and purification  
CC of clostridial toxin and to assay formulated clostridial toxin products  
CC including pharmaceuticals and cosmetics. The present sequence is fret  
CC substrate peptide used in the exemplification of the invention  
XX

SQ Sequence 21 AA;  
Query Match 100.0%; Score 93; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.4e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTTRIDEANQRATKML 19  
| | | | | | | | | | | | | | | | | | |  
Db 2 ADSNKTTRIDEANQRATKML 20

RESULT 3  
AAE36735  
ID AAE36735 standard; peptide; 24 AA.

XX  
AC AAE36735;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Fret substrate peptide #6 used in the invention.  
XX  
KW Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;  
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;  
KW cosmetic.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is  
FT given as Xaa in the sequence shown as SEQ ID NO: 90 in  
FT the sequence listing of the specification"  
FT  
FT Modified-site 24 /note= "Tetramethylrhodamine-modified Lysine; C-terminal  
FT amide; This residue is given as Xaa in the sequence shown  
FT as SEQ ID NO: 90 in the sequence listing of the  
FT specification"  
XX

WO2003020948-A2.

XX

PD 13-MAR-2003.

XX

PF 22-AUG-2002; 2002WO-US027145.

XX

PR 28-AUG-2001; 2001US-00942024.

XX

PA (ALLR ) ALLERGAN INC.

XX

PI Steward LE, Fernandez-Salas E, Aoki KR;

XX

DR WPI; 2003-290198/28.

XX

PS Botulinum serotype A/E substrate useful for assaying protease activity of

XX botulinum toxins, comprises donor fluorophore, acceptor and a clostridial

XX toxin recognition sequence that includes a cleavage site.

XX

PS Example 1; Page 115; 168pp; English.

XX

CC The present invention relates to novel clostridium toxin substrates. The

XX invention further relates to botulinum serotype A/E (BoNT/A/E) substrates

XX which comprise a donor fluorophore, an acceptor having an absorbance

XX spectrum overlapping the emission spectrum of the donor fluorophore and a

XX BoNT A or BoNT/E recognition sequence comprising a cleavage site, where

XX the cleavage site intervenes between the donor fluorophore and acceptor

XX and under the appropriate conditions, the resonance energy transfer is

XX exhibited between the donor and acceptor. Natural targets of clostridium

XX neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences

XX of the invention are useful in assaying for the protease activity of any

XX clostridial toxin including botulinum toxins of all serotypes and tetanus

XX toxins (TeNT) in a sample including bacterial, baculoviral and yeast

XX lysate, raw, cooked or processed foods, beverages, animal feed, soil

XX samples, water samples, cosmetics, tissue samples and beverage or food

XX samples. They are useful to assay a sample from a human or animal, for

XX e.g., exposed to clostridial toxin or having one or more symptoms of a

CC clostridial toxin including botulinum toxins of all serotypes and tetanus  
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast  
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil  
CC samples, water samples, cosmetics, tissue samples and beverage or food  
CC samples. They are useful to assay a sample from a human or animal, for  
CC e.g., exposed to clostridial toxin or having one or more symptoms of a  
CC clostridial toxin, to follow activity during production and purification  
CC of clostridial toxin and to assay formulated clostridial toxin products  
CC including pharmaceuticals and cosmetics. The present sequence is first  
CC substrate peptide used in the exemplification of the invention

XX  
SQ

Sequence 24 AA;

Query Match 100.0%; Score 93; DB 6; Length 24;

Best Local Similarity 100.0%; Pred. No. 2.8e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTRIDEANQRATKML 19

Db 2 ADSNKTRIDEANQRATKML 20

RESULT 4

AAW30099

ID AAW30099 standard; peptide; 26 AA.

XX AC AAW30099;

XX DT 06-APR-1998 (first entry)

XX DE Neurotransmitter secretion inhibitor #3.

XX KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;

XX KW excitation-secretory uncoupling peptide; catecholamine secretion;

XX KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;

XX KW synaptosomal associated protein; SNAP-25.

XX OS Homo sapiens.

XX PN W09734620-A1.

XX PD 25-SEP-1997.

XX PF 18-MAR-1997; 97WO-US004393.

XX PR 18-MAR-1996; 96US-0013599P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Montal M;

XX DR WPI; 1997-479986/44.

XX PT Excitation-secretory uncoupling peptide(s) for inhibiting

PT neuro:transmitter release - used particularly for treating muscle

PT spasticity, and for delivering drugs specifically to neural cells.

XX PS Claim 13; Page 31; 61pp; English.

XX CC This sequence corresponds to residues 181-206 of the human 25 kD

CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of

CC the invention. The agents of the invention inhibit secretion of

CC neurotransmitter from neuronal cells and is an excitation-secretory

CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which

CC correspond substantially to any one of AAW30097-W30102, or more generally

CC any (I) that inhibits 50% of catecholamine secretion from bovine

CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,

CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit

CC release of neurotransmitters from synaptic vesicles, specifically for

CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo

CC imaging of intracellular distribution of (I). Compounds for delivering

CC the drug to neural cells provide targeted drug delivery, e.g. of

CC substance P to brain tumours for induction of apoptosis. Unlike the

CC neurotoxins, (I) are not toxic or immunogenic and are more readily  
CC available. Their therapeutic effect lasts for several days or weeks, so  
CC lower doses or less frequent treatments are required

XX  
SQ

Sequence 26 AA;

Query Match 100.0%; Score 93; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 3e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTRIDEANQRATKML 19

Db 5 ADSNKTRIDEANQRATKML 23

RESULT 5

AAE36682

ID AAE36682 standard; peptide; 33 AA.

XX AC AAE36682;

XX DT 07-AUG-2003 (first entry)

XX DE Goldfish SNAP-25A peptide.

XX KW Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;

XX KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

XX KW TeNT; cosmetic.

XX OS Carassius auratus.

XX FH Key Location/Qualifiers

FT Cleavage-site 7. .8 /note= "BoNT/E sensitive cleavage site"

FT Cleavage-site 24. .25 /note= "BoNT/A sensitive cleavage site"

FT Cleavage-site 25. .26 /note= "BoNT/C sensitive cleavage site"

XX PN WO2003020948-A2.

XX PD 13-MAR-2003.

XX PF 22-AUG-2002; 2002WO-US027145.

XX PR 28-AUG-2001; 2001US-00942024.

XX PA (ALLR ) ALLERGAN INC.

XX PI Steward LE, Fernandez-Salas E, Aoki KR;

XX DR WPI; 2003-290198/28.

XX PT Botulinum serotype A/E substrate useful for assaying protease activity of

PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial

PT toxin recognition sequence that includes a cleavage site.

XX PS Disclosure; Page 42; 168pp; English.

XX CC The present invention relates to novel clostridium toxin substrates. The

CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates

CC which comprise a donor fluorophore, an acceptor having an absorbance

CC spectrum overlapping the emission spectrum of the donor fluorophore and a

CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where

CC the cleavage site intervenes between the donor fluorophore and acceptor

CC and under the appropriate conditions, the resonance energy transfer is

CC exhibited between the donor and acceptor. Natural targets of clostridium

CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences

CC of the invention are useful in assaying for the protease activity of any

CC clostridial toxin including botulinum toxins of all serotypes and tetanus

CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast

CC lysate, raw, cooked or processed foods, beverages, animal feed, soil

CC samples, water samples, cosmetics, tissue samples and beverage or food

CC samples. They are useful to assay a sample from a human or animal, for  
CC e.g., exposed to clostridial toxin or having one or more symptoms of a  
CC clostridial toxin, to follow activity during production and purification  
CC of clostridial toxin and to assay formulated clostridial toxin products  
CC including pharmaceuticals and cosmetics. The present sequence is goldfish  
CC SNAP-25A peptide used in the invention  
XX  
SQ Sequence 33 AA;

Query Match 100.0%; Score 93; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
Db 12 ADSNKTTRIDEANQRATKML 30

RESULT 6  
AAE36683  
ID AAE36683 standard; peptide; 33 AA.  
XX  
AC AAE36683;

DT 07-AUG-2003 (first entry)

XX Goldfish SNAP-25B peptide.

XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;  
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;  
KW TeNT; cosmetic.

XX Carassius auratus.

XX Key Location/Qualifiers

FT Cleavage-site 7. .8 /note= "BoNT/E sensitive cleavage site"

FT Cleavage-site 24. .25 /note= "BoNT/A sensitive cleavage site"

FT Cleavage-site 25. .26 /note= "BoNT/C sensitive cleavage site"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR ) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of  
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial  
PT toxin recognition sequence that includes a cleavage site.

XX Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The  
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates  
CC which comprise a donor fluorophore, an acceptor having an absorbance  
CC spectrum overlapping the emission spectrum of the donor fluorophore and a  
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where  
CC the cleavage site intervenes between the donor fluorophore and acceptor  
CC and under the appropriate conditions, the resonance energy transfer is  
CC exhibited between the donor and acceptor. Natural targets of clostridium  
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences  
CC of the invention are useful in assaying for the protease activity of any  
CC clostridial toxin including botulinum toxins of all serotypes and tetanus

CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast  
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil  
CC samples, water samples, cosmetics, tissue samples and beverage or food  
CC samples. They are useful to assay a sample from a human or animal, for  
CC e.g., exposed to clostridial toxin or having one or more symptoms of a  
CC clostridial toxin, to follow activity during production and purification  
CC of clostridial toxin and to assay formulated clostridial toxin products  
CC including pharmaceuticals and cosmetics. The present sequence is goldfish  
CC SNAP-25B peptide used in the invention  
XX

SQ Sequence 33 AA;

Query Match 100.0%; Score 93; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
Db 12 ADSNKTTRIDEANQRATKML 30

RESULT 7  
AAE36678  
ID AAE36678 standard; peptide; 33 AA.  
XX

AC AAE36678;

XX 07-AUG-2003 (first entry)

XX SNAP-25 peptide.

XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;  
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;  
KW cosmetic; mouse; rat.

XX Homo sapiens.

OS Mus musculus.

OS Rattus sp.

XX Key Location/Qualifiers

FT Cleavage-site 7. .8 /note= "BoNT/E sensitive cleavage site"

FT Cleavage-site 24. .25 /note= "BoNT/A sensitive cleavage site"

FT Cleavage-site 25. .26 /note= "BoNT/C sensitive cleavage site"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

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XX WPI; 2003-290198/28.

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PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial  
PT toxin recognition sequence that includes a cleavage site.

XX Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The  
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates  
CC which comprise a donor fluorophore, an acceptor having an absorbance  
CC spectrum overlapping the emission spectrum of the donor fluorophore and a  
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where  
CC the cleavage site intervenes between the donor fluorophore and acceptor



CC and under the appropriate conditions, the resonance energy transfer is  
CC exhibited between the donor and acceptor. Natural targets of clostridium  
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences  
CC of the invention are useful in assaying for the protease activity of any  
CC clostridial toxin including botulinum toxins of all serotypes and tetanus  
CC toxins (Tent) in a sample including bacterial, baculoviral and yeast  
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil  
CC samples, water samples, cosmetics, tissue samples and beverage or food  
CC samples. They are useful to assay a sample from a human or animal, for  
CC e.g., exposed to clostridial toxin or having one or more symptoms of a  
CC clostridial toxin, to follow activity during production and purification  
CC of clostridial toxin and to assay formulated clostridial toxin products  
CC including pharmaceuticals and cosmetics. The present sequence is SNAP-25  
CC peptide used in the invention

XX Sequence 33 AA;

Query Match 100.0%; Score 93; DB 6; Length 33;

Best Local Similarity 100.0%; Pred. No. 4e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
DB 12 ADSNKTTRIDEANQRATKML 30  
|||||

RESULT 8

AAW30097  
ID AAW30097 standard; peptide; 37 AA.

XX AAW30097;

XX 06-APR-1998 (first entry)

XX Neurotransmitter secretion inhibitor #1.

XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;  
KW excitation-secretory uncoupling peptide; catecholamine secretion;  
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
KW synaptosomal associated protein; SNAP-25.

XX Homo sapiens.

XX WO9734620-A1.

XX 25-SEP-1997.

XX 18-MAR-1997; 97WO-US004393.

XX 18-MAR-1996; 96US-0013599P.

XX (REGC ) UNIV CALIFORNIA.

XX Montal M;

XX WPI; 1997-479986/44.

XX Excitation-secretory uncoupling peptide(s) for inhibiting  
PT neurotransmitter release - used particularly for treating muscle  
PT spasticity, and for delivering drugs specifically to neural cells.

XX Claim 1; Page 30; 61pp; English.

CC This sequence corresponds to residues 170-206 of the human 25 kD  
CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of  
CC the invention. The agents of the invention inhibit secretion of  
CC neurotransmitter from neuronal cells and is an excitation-secretory  
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which  
CC correspond substantially to any one of AAW30097-W30102, or more generally  
CC any (I) that inhibits 50% of catecholamine secretion from bovine  
CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,  
CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit  
CC release of neurotransmitters from synaptic vesicles, specifically for

CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo  
CC imaging of intracellular distribution of (I). Compounds for delivering  
CC the drug to neural cells provide targeted drug delivery, e.g. of  
CC substance P to brain tumours for induction of apoptosis. Unlike the  
CC neurotoxins, (I) are not toxic or immunogenic and are more readily  
CC available. Their therapeutic effect lasts for several days or weeks, so  
CC lower doses or less frequent treatments are required

XX Sequence 37 AA;

Query Match 100.0%; Score 93; DB 2; Length 37;

Best Local Similarity 100.0%; Pred. No. 4.5e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
DB 16 ADSNKTTRIDEANQRATKML 34  
|||||

RESULT 9

AAW66823  
ID AAW66823 standard; peptide; 70 AA.

XX AAW66823;

XX 15-AUG-1996 (first entry)

XX SNAP-25 residues 137-206.

XX VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;  
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;  
KW antibody; detection; assay.

XX Synthetic.

XX WO9533850-A1.

XX 14-DEC-1995.

XX 02-JUN-1995; 95WO-GB001279.

XX 03-JUN-1994; 94GB-00011138.

XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.

XX Shone CC, Hallis B, James BAF, Quinn CP;

XX WPI; 1996-040249/04.

XX Assay for botulinum or tetanus toxin - by combining test cpd. with  
PT substrate which is cleaved by the toxin, and antibody specific for the  
PT cleaved but not uncleaved substrate.

XX Example 4; Page 19; 48pp; English.

XX The botulinum neurotoxins possess highly specific zinc-endopeptidase  
CC activities within their light sub-units. Depending on the neurotoxin type  
CC these act to cleave small proteins within the nerve cell which are  
CC involved in neurotransmitter release. Antibodies are used in assays which  
CC detect cleaved but not uncleaved substrate. Assays for botulinum types A  
CC and E use the present sequence as a substrate. The sequence is SNAP-25  
CC protein, residues 137-206

XX Sequence 70 AA;

Query Match 100.0%; Score 93; DB 2; Length 70;

Best Local Similarity 100.0%; Pred. No. 9.3e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19  
DB 49 ADSNKTTRIDEANQRATKML 67  
|||||

## RESULT 10

AA0151584  
ID AAB15584 standard; peptide; 86 AA.

XX AC AAB15584;

XX DT 02-MAR-2001 (first entry)

XX DE Human SNAP-25 N-terminal peptide #4.

XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;  
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;  
KW neurodegenerative disorder.

XX OS Homo sapiens.

XX PN WO200064932-A1.

XX PD 02-NOV-2000.

XX PF 18-FEB-2000; 2000WO-ES000058.

XX PR 23-APR-1999; 99ES-00000844.

XX PA (LIPO-) LIPOTEC SA.

XX PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;  
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;  
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;  
PI Perez Paya E;

XX DR WPI; 2001-007091/01.

XX PT New peptides containing amino acid sequences from known proteins for  
PT treatment of neurological disorders.

XX PS Claim 16; Page 32-33; 40pp; Spanish.

XX CC The invention relates to new peptides comprising 3-30 contiguous amino  
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated  
CC protein 25). The peptides AAB15581-B15586 represent examples of the  
CC peptides of the invention. The peptides have neuronal exocytosis  
CC inhibitory activity and are used for treatment of facial wrinkles and  
CC asymmetry and pathological neuronal exocytosis-mediated pathological  
CC disorders and alterations manifested e.g. by spasms and neurological and  
CC neurodegenerative disorders

XX SQ Sequence 86 AA;

Query Match 100.0%; Score 93; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRTKML 19

Db 65 ADSNKTTRIDEANQRTKML 83

## RESULT 11

AA015165  
ID AAO15165 standard; peptide; 116 AA.

XX AC AAO15165;

XX DT 02-SEP-2002 (first entry)

XX DE Clostridial neurotoxin protease substrate peptide 4.

XX KW Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;  
KW fluorescence resonant energy transfer assay; quenched-signal;  
KW clostridial neurotoxin detection; food.

XX OS Unidentified.  
XX FT Key Modified-site 1 Location/Qualifiers  
XX FT Cleavage-site 89..90 /note= "S-fluoresceinyl-cysteine"  
XX FT Cleavage-site 106..107 /note= "The peptide is cleaved between these two residues  
XX FT by type E Clostridium botulinum neurotoxin"  
XX FT by type A Clostridium botulinum neurotoxin"

XX PN WO200225284-A2.

XX PD 28-MAR-2002.

XX PF 25-SEP-2001; 2001WO-US030188.

XX PR 25-SEP-2000; 2000US-0235050P.

XX PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX PI Schmidt JJ, Stafford RG;

XX DR WPI; 2002-499829/53.

XX PT Substrate useful in e.g. an assay for the protease activity of  
XX clostridial neurotoxin, comprises modified peptide or protein.

XX PS Claim 22; Page 16; 48pp; English.

XX CC The invention comprises clostridial neurotoxin substrate peptides which  
XX can serve as fluorescence resonant energy transfer assay (FRET) or  
XX quenched-signal substrates in assays for the proteolytic activities of  
XX clostridial neurotoxins. The invention further comprises Clostridium  
XX botulinum neurotoxin substrate peptides that can serve as immobilised  
XX substrates (i.e. bound to a solid phase) in assays for the proteolytic  
XX activities of clostridial neurotoxins. The clostridial (including the  
XX Clostridium botulinum) neurotoxin substrate peptides are useful for  
XX detecting the presence of clostridial neurotoxins in a sample (e.g. food  
XX or an environmental sample). The present amino acid sequence represents a  
XX clostridial neurotoxin substrate peptide of the invention

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 93; DB 5; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.6e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRTKML 19

Db 94 ADSNKTTRIDEANQRTKML 112

## RESULT 12

AAW30103  
ID AAW30103 standard; peptide; 206 AA.

XX AC AAW30103;

XX DT 06-APR-1998 (first entry)

XX DE Synaptosomal associated protein.

XX KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;  
KW excitation-secretory uncoupling peptide; catecholamine secretion;  
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
KW synaptosomal associated protein; SNAP-25.

XX OS Homo sapiens.

XX PN WO9734620-A1.

XX 25-SEP-1997.  
PD  
XX  
XX 18-MAR-1997; 97WO-US004393.  
PF  
XX  
XX 18-MAR-1996; 96US-0013599P.  
PR  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX  
XX Montal M;  
PI  
XX  
XX WPI; 1997-479986/44.  
DR  
XX  
XX Excitation-secretory uncoupling peptide(s) for inhibiting  
PT neuro:transmitter release - used particularly for treating muscle  
PT spasticity, and for delivering drugs specifically to neural cells.  
XX  
XX Disclosure; Page 27-28; 61pp; English.  
PS  
XX  
XX This sequence represents the human 25 kD synaptosomal associated protein  
CC (SNAP-25), which is an inhibitory agent of the invention. The agents of  
CC the invention inhibit secretion of neurotransmitter from neuronal cells  
CC and is an excitation-secretory uncoupling peptide (I) of at least 20  
CC amino acids (aa) all of which correspond substantially to any one of  
CC AAW30097-W30102, or more generally any (I) that inhibits 50% of  
CC catecholamine secretion from bovine chromaffin cells at a concentration  
CC of 10 microM, especially 0.25 microM, or less. (I) are used, as a  
CC replacement for Clostridium toxin, to inhibit release of  
CC neurotransmitters from synaptic vesicles, specifically for reducing  
CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of  
CC intracellular distribution of (I). Compounds for delivering the drug to  
CC neural cells provide targeted drug delivery, e.g. of substance P to brain  
CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not  
CC toxic or immunogenic and are more readily available. Their therapeutic  
CC effect lasts for several days or weeks, so lower doses or less frequent  
CC treatments are required  
XX  
SQ Sequence 206 AA;  
  
Query Match 100.0%; Score 93; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ADSNKTTRIDEANQRATKML 19  
Db 185 ADSNKTTRIDEANQRATKML 203  
  
RESULT 13  
AAW43426  
ID AAW43426 standard; protein; 206 AA.  
XX  
AC AAW43426;  
XX  
DT 27-APR-1998 (first entry)  
XX  
XX Mouse synaptosomal-associated protein-25.  
DE  
XX Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;  
KW neurotransmitter; presynaptic membrane; central nervous system; tumour;  
KW neurodegenerative disease; hormonal disorder; immunological disorder.  
XX  
OS Mus sp.  
XX  
XX US5693476-A.  
PN  
XX 02-DEC-1997.  
PD  
XX 24-FEB-1995; 95US-00393985.  
PF  
XX 24-FEB-1995; 95US-00393985.  
PR  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA

XX Scheller RH;  
PI  
XX WPI; 1998-031743/03.  
DR  
XX N-PSDB; AAV01554.  
XX  
PT Screening assay for modulators of syntaxin binding - using peptide  
PT comprising binding site of syntaxin, for identifying drugs useful for  
PT treating CNS disorders, neuro-degenerative diseases, etc.  
XX  
XX Disclosure; Col 67-72; 57pp; English.  
PS  
XX  
XX This amino acid sequence represents the mouse synaptosomal-associated  
CC protein of 25 kD (SNAP-25). The invention relates to a method for  
CC identifying a compound capable of affecting the binding of a syntaxin-  
CC binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to  
CC syntaxin. The method comprises measuring the effect of the test compound  
CC on the extent of binding between the SBP and the SBP-binding site on  
CC syntaxin. The method can be used for identifying drugs capable of  
CC inhibiting or stimulating neurotransmitter release at the active zones of  
CC presynaptic membranes, which may be useful for treating CNS disorders,  
CC affective or psychotic disorders, neurodegenerative diseases, hormonal or  
CC immunological disorders or tumours  
XX  
SQ Sequence 206 AA;  
  
Query Match 100.0%; Score 93; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ADSNKTTRIDEANQRATKML 19  
Db 185 ADSNKTTRIDEANQRATKML 203  
  
RESULT 14  
AAW79198  
ID AAW79198 standard; protein; 206 AA.  
XX  
AC AAW79198;  
XX  
DT 25-NOV-1998 (first entry)  
XX  
XX Mouse SNAP-25 polypeptide.  
DE  
XX  
XX Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking;  
KW calcium-regulated secretion; secretory vesicle; secretory process; brain;  
KW neurotransmitter release; presynaptic membrane; CNS disorder; depression;  
KW Parkinson's disease; endocrine system; hormonal imbalance; cell division;  
KW thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;  
KW immune system; antigen processing; immunomodulator; viral processing;  
KW central nervous system; vesicular release; affective disorder; human;  
KW anti-tumour application; membrane trafficking regulation; mouse.  
XX  
OS Mus sp.  
XX  
XX WO9838210-A2.  
PN  
XX  
XX 03-SEP-1998.  
PD  
XX 26-FEB-1998; 98WO-US003789.  
PF  
XX  
XX 26-FEB-1997; 97US-0039159P.  
PR  
XX  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA  
XX  
XX Bean AJ, Scheller RH;  
PI  
XX WPI; 1998-481140/41.  
DR  
XX N-PSDB; AAV57558.  
XX  
XX New isolated Hrs-2 nucleotidase - used in assays to identify compounds  
PT capable of modulating calcium-regulatory secretion of secretory vesicles,  
PT



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OM protein - protein search, using sw model

Run on: March 9, 2004, 10:58:06 ; Search time 10.2162 Seconds  
(without alignments)  
91.743 Million cell updates/sec

Title: US-10-030-485A-5

Perfect score: 89

Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	204	1 SN2A_CARAU	P36977 carassius a
2	89	100.0	206	1 SN25_HUMAN	P13795 homo sapien
3	80	89.9	203	1 SN2B_CARAU	P36978 carassius a
4	60	67.4	210	1 SN25_TORNA	P36976 torpedo mar
5	55	61.8	211	1 SN23_HUMAN	O00161 homo sapien
6	45	50.6	212	1 SN25_DROME	P36975 drosophila
7	43	48.3	1353	1 CVA9_HUMAN	O60503 homo sapien
8	41	46.1	298	1 HCD1_CAEEL	P34439 caenorhabdi
9	41	46.1	377	1 Y392_CHLTR	P36427 chlamydia t
10	41	46.1	437	1 YSH8_CAEEL	Q09949 caenorhabdi
11	40	44.9	320	1 MCH_METTH	O26867 methanobact
12	40	44.9	442	1 BNB_DROME	P29746 drosophila
13	40	44.9	499	1 GAB_LYMT	P26714 lymanaea sta
14	40	44.9	550	1 DBP2_SCHPO	P24782 schizosacch
15	40	44.9	580	1 5NTD_BOOMI	P52307 boophilus m
16	40	44.9	2867	1 RBP2_PLAVB	Q00799 plasmodium
17	39.5	44.4	668	1 VNCS_FPV19	P24842 feline panl
18	39.5	44.4	668	1 VNCS_PAVCN	P12929 canine parv
19	39	43.8	267	1 MLF1_MOUSE	Q9QWV4 mus musculu
20	39	43.8	277	1 URED_RHINE	P42888 rhizobium m
21	39	43.8	294	1 CAL2_PARTE	Q94715 paramecium
22	39	43.8	605	1 GOX_TALFL	Q92452 talaromyces
23	39	43.8	1798	1 LMB2_HUMAN	P55268 homo sapien
24	39	43.8	1799	1 LMB2_MOUSE	Q61292 mus musculu
25	39	43.8	1801	1 LMB2_RAT	P15800 rattus norv
26	39	43.8	2164	1 POLG_HRV89	P07210 h genome po
27	39	43.8	3255	1 POLG_LMV0	P31999 l genome po
28	39	43.8	3255	1 POLG_LMVE	P89876 l genome po
29	39	43.8	7389	1 BPA1_MOUSE	Q912u6 mus musculu
30	38.5	43.3	621	1 RFA1_YEAST	P22336 saccharomyc
31	38.5	43.3	640	1 DNAK_PORGI	Q92ad3 porphyronon
32	38	42.7	133	1 ATPC_CYACA	Q9tm40 cyanidium c
33	38	42.7	184	1 ARF2_SCHPO	Q9y7z2 schizosacch

34	38	42.7	204	1 IPP2_RAT	P50411 rattus norv
35	38	42.7	243	1 GTT2_HUMAN	P30712 homo sapien
36	38	42.7	328	1 PTA_CLOTS	Q59330 clostridium
37	38	42.7	484	1 PAP2_XENLA	P51005 xenopus lae
38	38	42.7	502	1 C72A_ARATH	Q91vd2 arabidopsis
39	38	42.7	513	1 FLAB_HELPJ	Q9zmv8 helicobacte
40	38	42.7	513	1 FLAB_HELPY	Q07911 helicobacte
41	38	42.7	587	1 GOX_PENAG	P81156 penicillium
42	38	42.7	704	1 MID2_SCHPO	Q9p7y8 schizosacch
43	38	42.7	785	1 YG51_YEAST	P50089 saccharomyc
44	38	42.7	3163	1 POLG_TUMVQ	Q02597 t genome po
45	38	42.7	3164	1 POLG_TUMVJ	P89509 t genome po

#### ALIGNMENTS

RESULT 1  
SN2A\_CARAU  
ID SN2A\_CARAU STANDARD; PRT; 204 AA.  
AC P36977;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Synaptosomal-associated protein 25A (SNAP-25A).  
GN SNAP-A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retina;  
RX MEDLINE=94068448; PubMed=8248151;  
RA Risinger C., Larhammar D.;  
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).  
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.  
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.  
CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
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CC -----  
CC EMBL; L22973; AAA16537.1; -.  
CC PIR; I50480; I50480.  
CC InterPro; IPR000928; SNAP-25.  
CC InterPro; IPR000727; T-SNARE.  
CC Pfam; PF00835; SNAP-25; 1.  
CC Pfam; PF05739; SNARE; 1.  
CC SMART; SM00397; t-SNARE; 2.  
CC PROSITE; PS50192; T-SNARE; 2.  
KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.  
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.  
FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOMOLOGY 2.  
FT DOMAIN 85 92 CYS-RICH.  
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;  
  
Query Match 100.0%; Score 89; DB 1; Length 204;  
Best Local Similarity 100.0%; Pred. No. 4,3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 RIMEXADSNKTRIDEANQ 18  
Db 178 RIMEXADSNKTRIDEANQ 195

RESULT 2

SN25\_HUMAN STANDARD; PRT; 206 AA.  
AC P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).  
GN SNAP25 OR SNAP.

OS Homo sapiens (Human),  
OS Macaca mulatta (Rhesus macaque),  
OS Mus musculus (Mouse),  
OS Rattus norvegicus (Rat), and  
OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606, 9544, 10090, 10116, 9031;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
RC SPECIES=Human; TISSUE=Brain;  
RX MEDLINE=94156217; PubMed=8112622;  
RA Bark I.C., Wilson M.C.;  
RT "Human cDNA clones encoding two different isoforms of the nerve  
terminal protein SNAP-25.";  
RL Gene 139:291-292(1994).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).  
RC SPECIES=Human; TISSUE=Brain;  
RX MEDLINE=94333829; PubMed=8056350;  
RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;  
RT "Cloning and sequence analysis of the human SNAP25 cDNA.";  
RL Gene 145:313-314(1994).  
RN [3]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC SPECIES=Human; TISSUE=Skeletal muscle;  
RX MEDLINE=96332494; PubMed=8760387;  
RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,  
RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,  
RA Frenkel M.J., Ward C.W.;  
RT "Insulin-responsive tissues contain the core complex protein SNAP-25  
(synaptosomal-associated protein 25) A and B isoforms in addition to  
syntaxin 4 and synaptobrevins 1 and 2.";  
RL Biochem. J. 317:945-954(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human;  
RX MEDLINE=21638749; PubMed=11780052;  
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Hunt J.B., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.I., McConachie L.J., McLay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RL "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Human; TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=M.mullatta; TISSUE=Hippocampus;  
RA Jensen M.J., Smith L.A.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Mouse; STRAIN=BALB/c;  
RX MEDLINE=90078337; PubMed=2592413;  
RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,  
RA Bloom F.E., Wilson M.C.;  
RT "The identification of a novel synaptosomal-associated protein,  
SNAP-25, differentially expressed by neuronal subpopulations.";  
RL J. Cell Biol. 109:3039-3052(1989).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Mouse; STRAIN=ILS, and ISS;  
RX MEDLINE=21363810; PubMed=11471062;  
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,  
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;  
RT "High-throughput sequence identification of gene coding variants  
within alcohol-related QTLs.";  
RL Mamm. Genome 12:657-663(2001).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).  
RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaído I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;  
RA Strausberg R.L.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
RC SPECIES=Cat;  
RA Kataoka M.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).  
RC SPECIES=Cat; TISSUE=Brain;  
RA Cho A.R., You K.H.;  
RL "Cloning of the SNAP-25 gene from a rat brain cDNA library";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).  
RC SPECIES=Cat; TISSUE=Brain;  
RX MEDLINE=99155074; PubMed=10037470;  
RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;  
RT "SNARE complex proteins, including the cognate pair VAMP-2 and  
RT syntaxin-4, are expressed in cultured oligodendrocytes";  
RL J. Neurochem. 72:988-998 (1999).  
RN [14]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Chicken; TISSUE=Retina;  
RX MEDLINE=91126080; PubMed=1992470;  
RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,  
RA Wilson M.C.;  
RT "Expression of a conserved cell-type-specific protein in nerve  
RT terminals coincides with synaptogenesis";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789 (1991).  
RN [15]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC SPECIES=Chicken;  
RX MEDLINE=93389738; PubMed=8377193;  
RA Bark I.C.;  
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon  
RT encoding distinct isoforms of the protein";  
RL J. Mol. Biol. 233:67-76 (1993).  
RN [16]  
RP PALMITOYLATION.  
RC SPECIES=Cat;  
RX MEDLINE=93100552; PubMed=1281490;  
RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;  
RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major  
RT methionine-rich polypeptide in rapid axonal transport and a major

Query Match 100.0%; Score 89; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
Db |||||  
180 RIMEKADSNKTRIDEANQ 197

RESULT 3  
SN2B\_CARAU

ID SN2B\_CARAU STANDARD; PRT; 203 AA.  
AC P36978;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Synaptosomal-associated protein 25B (SNAP-25B).  
GN SNAP-B.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retina;  
RX MEDLINE=94068448; PubMed=8248151;  
RA Risinger C., Larhammar D.;  
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid  
RT goldfish.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602 (1993).  
CC -!- FUNCTION: May play an important role in the synaptic function of  
CC specific neuronal systems. Associates with proteins involved in  
CC vesicle docking and membrane fusion.  
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of  
CC the nerve terminal.  
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus,  
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and  
CC granule cells of the cerebellum.  
CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
CC -----  
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CC -----  
CC EMBL; L22976; AAA16538.1; -  
DR PIR; I50481; I50481.  
DR InterPro; IPR000928; SNAP-25.  
DR InterPro; IPR000727; T-SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR Pfam; PF05739; SNARE; 1.  
DR SMART; SM00397; t-SNARE; 2.  
DR PROSITE; PS50192; T-SNARE; 2.  
KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.  
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.  
FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOMOLOGY 2.  
FT DOMAIN 85 92 CYS-RICH.  
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 203 AA; 22664 MW; 8DFBEBED37D6D7 CRC64;  
Query Match 89.9%; Score 80; DB 1; Length 203;  
Best Local Similarity 88.9%; Pred. No. 1.2e-05;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
Db |||||  
177 RIMEKADSNKTRIDEANQ 194

RESULT 4  
SN25\_TORMA  
ID SN25\_TORMA STANDARD; PRT; 210 AA.  
AC P36976;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Synaptosomal-associated protein 25 (SNAP-25).  
OS Torpedo marmorata (Marbled electric ray).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squalea; Hynostomalea; Pristiorajae; Batoidae;  
 OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.  
 OX NCBI\_TaxID=7788;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Electric lobe;  
 RX MEDLINE=94043281; PubMed=8226991;  
 RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,  
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;  
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa  
 (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";  
 RL J. Biol. Chem. 268:24408-24414(1993).  
 CC -!- FUNCTION: May play an important role in the synaptic function of  
 CC specific neuronal systems. Associates with proteins involved in  
 CC vesicle docking and membrane fusion.  
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of  
 CC the nerve terminal.  
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
 CC  
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 CC  
 DR EMBL; L22020; AAA49284.1; -;  
 DR PIR; I50552; I50552.  
 DR InterPro; IPR000928; SNAP-25.  
 DR InterPro; IPR000727; t-SNARE.  
 DR Pfam; PF00835; SNAP-25; 1.  
 DR Pfam; PF05739; SNARE; 1.  
 DR SMART; SM00397; t-SNARE; 2.  
 DR PROSITE; PS50192; t-SNARE; 2.  
 KW Synaptosome; Neurone; Repeat; Coiled coil.  
 FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOMOLOGY 1.  
 FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOMOLOGY 2.  
 FT DOMAIN 88 96 CVS-RICH.  
 SQ SEQUENCE 210 AA; 23652 MW; 58FE471A9234B8B1 CRC64;  
 Query Match 67.4%; Score 60; DB 1; Length 210;  
 Best Local Similarity 66.7%; Pred. No. 0.018;  
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RIMEKADSNKTRIDEANQ 18  
 Db 187 RIVKGDMMKARIDEANK 204  
 RESULT 5  
 SN23\_HUMAN STANDARD; PRT; 211 AA.  
 ID O00161; O00162; Q13602;  
 AC 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Synaptosomal-associated protein 23 (SNAP-23) (Vesicle-membrane fusion  
 DE protein SNAP-23).  
 GN SNAP23.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).  
 RC TISSUE=B-cell;  
 RX MEDLINE=96278745; PubMed=8663154;  
 RA Ravichandran V., Chawla A., Roche P.A.;  
 RT "Identification of a novel syntaxin- and synaptobrevin/VAMP-binding  
 RT protein, SNAP-23, expressed in non-neuronal tissues.";

RL J. Biol. Chem. 271:13300-13303(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-23A AND SNAP-23B).  
 RC TISSUE=Neutrophils;  
 RX MEDLINE=97224437; PubMed=9070898;  
 RA Mollinedo F., Lazo P.A.;  
 RT "Identification of two isoforms of the vesicle-membrane fusion protein  
 RT SNAP-23 in human neutrophils and HL-60 cells.";  
 RL Biochem. Biophys. Res. Commun. 231:808-812(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RA Nadal M., Area E., Mollinedo F., Estivill X., Lazo P.A.;  
 RT "Exon organization and chromosomal localization of human synaptosomal  
 RT associated protein-23 (SNAP-23) gene and generation of isoforms by  
 RT alternative splicing.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).  
 RC TISSUE=Cervix, Placenta, and Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: ESSENTIAL COMPONENT OF THE HIGH AFFINITY RECEPTOR FOR  
 CC THE GENERAL MEMBRANE FUSION MACHINERY AND AN IMPORTANT REGULATOR  
 CC OF TRANSPORT VESICLE DOCKING AND FUSION.  
 CC -!- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS AND  
 CC SYNAPTOBREVS/VAMPS.  
 CC -!- SUBCELLULAR LOCATION: MAINLY LOCALIZED TO THE PLASMA MEMBRANE.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=SNAP-23a;  
 CC IsoId=O00161-1; Sequence=Displayed;  
 CC Name=SNAP-23b;  
 CC IsoId=O00161-2; Sequence=VSP\_006187, VSP\_006188;  
 CC -!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS WHERE FOUND IN  
 CC PLACENTA.  
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
 CC  
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 CC  
 DR EMBL; U55936; AAC50537.1; -;  
 DR EMBL; Y09567; CAA70760.1; -;  
 DR EMBL; Y09568; CAA70761.1; -;  
 DR EMBL; AJ011915; CAA09864.1; -;  
 DR EMBL; BC000148; AAH00148.1; -;  
 DR EMBL; BC003686; AAH03686.1; -;  
 DR EMBL; BC022890; AAH22890.1; -;  
 DR PIR; JC5296; JC5296.

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DR PIR; JC5297; JC5297.
DR Genew; HGNC:11131; SNAP23.
DR MIM; 602534; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005803; C:secretory vesicle; TAS.
DR GO; GO:0006944; P:membrane fusion; TAS.
DR GO; GO:0006903; P:nonselective vesicle targeting; TAS.
DR GO; GO:0006892; P:post-Golgi transport; TAS.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
KW Protein transport; Synaptosome; Coiled coil; Alternative splicing;
KW Membrane; Repeat.
FT DOMAIN 14 76 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 146 208 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT VARSPLIC 89 89 R -> S (in isoform SNAP-23b).
FT VARSPLIC 90 142 /FTid=VSP 006187.
FT VARSPLIC 135 135 Missing (in isoform SNAP-23b).
FT VARSPLIC 211 AA; 23354 MW; AC378E9786C3A239 CRC64;
Query Match 61.8%; Score 55; DB 1; Length 211;
Best Local Similarity 64.7%; Pred. No. 0.11;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
DB 186 RITDKADTNRDRIDIAN 202

RESULT 6
SN25_DROME
ID SN25_DROME STANDARD; PRT; 212 AA.
AC P36975;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25).
GN SNAP25.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=94043281; PubMed=8226991;
RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
RL J. Biol. Chem. 268:24408-24414(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97417485; PubMed=9272858;
RA Risinger C., Deitcher D.L., Lundell I., Schwarz T.L., Larhammar D.;
RT "Complex gene organization of synaptic protein SNAP-25 in Drosophila
RT melanogaster.";
RL Gene 194:169-177(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=22426071; PubMed=12537574;
RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
RA Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
RA Yasuhara J.C., Wakimoto B.T., Myers B.W., Celniker S.E., Rubin G.M.,
RA Karpen G.H.;
RT "Heterochromatic sequences in a Drosophila whole-genome shotgun

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RT assembly.";
RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).
CC -!- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -!- TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GANGLIA.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
-----
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CC or send an email to license@isb-sib.ch).
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CC EMBL; L22021; AAA16059.1; -.
CC EMBL; U81153; AAB39757.1; -.
CC EMBL; U81147; AAB39757.1; JOINED.
CC EMBL; U81148; AAB39757.1; JOINED.
CC EMBL; U81149; AAB39757.1; JOINED.
CC EMBL; U81150; AAB39757.1; JOINED.
CC EMBL; U81151; AAB39757.1; JOINED.
CC EMBL; U81152; AAB39757.1; JOINED.
CC FlyBase; FBgn0011288; Snap25.
CC GO; GO:0005886; C:plasma membrane; NAS.
CC GO; GO:0005486; F:t-SNARE activity; NAS.
CC GO; GO:0007269; P:neurotransmitter secretion; NAS.
CC GO; GO:0016081; P:synaptic vesicle docking; NAS.
CC GO; GO:0016083; P:synaptic vesicle fusion; NAS.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR00727; T-SNARE.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS50192; T-SNARE; 2.
KW Synaptosome; Neurone; Repeat; Coiled coil.
FT DOMAIN 26 88 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 148 210 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 91 99 CYS-RICH.
SQ SEQUENCE 212 AA; 23685 MW; BDC90649A1AF3AC8 CRC64;

Query Match 50.6%; Score 45; DB 1; Length 212;
Best Local Similarity 55.6%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
DB 188 RINRKGESNEARIANQ 205

RESULT 7
CYA9_HUMAN
ID CYA9_HUMAN STANDARD; PRT; 1353 AA.
AC O60503; O60273; Q9BWT4; Q9UGP2;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adenylate cyclase, type IX (EC 4.6.1.1) (ATP pyrophosphate-lyase)
DE (Adenylate cyclase).
DE ADCY9 OR KIAA0520.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98292499; PubMed=9628827;
RA Hacker B.M., Tomlinson J.E., Wayman G.A., Sultana R., Chan G.,

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FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 15 15 T -> K (IN REF. 2).  
FT CONFLICT 37 39 SGT -> HXG (IN REF. 2).  
SQ SEQUENCE 580 AA; 63460 MW; 588EEF2014071AB7 CRC64;  
  
Query Match 44.9%; Score 40; DB 1; Length 580;  
Best Local Similarity 35.3%; Pred. No. 78;  
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 RIMEKADSNKTRIDEAN 17  
Db :: | | : | : | |  
339 KVLDDGDKNRCLDECN 355

Search completed: March 9, 2004, 11:08:09  
Job time : 11.2162 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:04:36 ; Search time 13.1351 Seconds  
(without alignments)  
131.818 Million cell updates/sec

Title: US-10-030-485A-5  
Perfect score: 89  
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	204	2 I50480	synapse protein SN
2	89	100.0	206	2 A37861	synaptosomal-assoc
3	89	100.0	206	2 I53735	nerve terminal pro
4	89	100.0	206	2 I67823	nerve terminal pro
5	89	100.0	206	2 A33623	synaptosomal-assoc
6	80	89.9	203	2 I50481	synapse protein SN
7	60	67.4	210	2 I50552	synapse protein -
8	59	66.3	210	2 JC5512	SNARE protein 23 -
9	55	61.8	158	2 JC5297	vesicle-membrane f
10	55	61.8	211	2 JC5296	vesicle-membrane f
11	54	60.7	29	2 A49708	synaptosomal-assoc
12	50	56.2	234	2 T26553	hypothetical prote
13	45	50.6	1138	2 T24635	hypothetical prote
14	43	48.3	401	2 E81436	transmembrane tran
15	43	48.3	480	2 T18905	hypothetical prote
16	42	47.2	173	2 S38231	hypothetical prote
17	41	46.1	141	2 T33983	hypothetical prote
18	41	46.1	285	2 AD3576	fusaric acid resis
19	41	46.1	298	1 A40743	3-hydroxyacyl-CoA
20	41	46.1	318	2 B90399	probable acyl-coen
21	41	46.1	377	2 F71520	hypothetical prote
22	41	46.1	393	2 T16046	hypothetical prote
23	41	46.1	554	2 F86244	hypothetical prote
24	41	46.1	575	2 F96966	hypothetical prote
25	41	46.1	642	2 G90551	methyle-accepting c
26	41	46.1	2541	2 T29340	lipoprotein [impor
27	40.5	45.5	228	2 B89776	hypothetical prote
28	40	44.9	300	2 H75200	capsular polysacch
29	40	44.9	300	2 D71234	hypothetical prote

30 40 44.9 320 2 D69203 methenyltetrahydro  
31 40 44.9 362 2 T49090 hypothetical prote  
32 40 44.9 409 2 D90182 LPS biosynthesis p  
33 40 44.9 441 2 A43555 GAP-43-related pro  
34 40 44.9 499 2 S17785 gamma-aminobutyric  
35 40 44.9 550 1 S14048 RNA helicase dbp2  
36 40 44.9 689 2 T25202 hypothetical prote  
37 40 44.9 1031 2 A12589 DNA polymerase I  
38 40 44.9 1031 2 B97372 DNA polymerase I  
39 40 44.9 1252 2 B42771 reticulocyte-bind  
40 40 44.9 1254 2 E86160 hypothetical prote  
41 40 44.9 1787 2 AG1360 probable tape-meas  
42 39.5 44.4 668 1 UYPVCP noncapsid protein  
43 39.5 44.4 668 1 UYPVFP noncapsid protein  
44 39 43.8 117 2 G82982 conserved hypothet  
45 39 43.8 225 2 T28319 ORF MSV158 probabl

ALIGNMENTS

RESULT 1

I50480  
synapse protein SNAP-25 - goldfish  
C;Species: Carassius auratus (goldfish)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C;Accession: I50480  
R;Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A;Reference number: A49632; MUID:94068448; PMID:8248151  
A;Accession: I50480  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-204 <RIS>  
A;Cross-references: GB:L22973; NID:g349426; PIDN:AAA16537.1; PID:g349427  
C;Genetics:  
A;Gene: SNAP-25

Query Match 100.0%; Score 89; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 178 RIMEKADSNKTRIDEANQ 195

RESULT 2

A37861  
synaptosomal-associated 25K protein - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 21-Jul-2000  
C;Accession: A37861  
R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991  
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coinci  
A;Reference number: A37861; MUID:91126080; PMID:1992470  
A;Accession: A37861  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-206 <CAT>  
A;Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 100.0%; Score 89; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 3  
I53735  
nerve terminal protein - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I53735  
R:Bark, I.C.; Wilson, M.C.  
Gene 139, 291-292, 1994  
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein  
A:Reference number: I53735; MUID:94156217; PMID:8112622  
A:Accession: I53735  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-206 <RES>  
A:Cross-references: GB:L19760; NID:g307425; PIDN:AAC37545.1; PID:g307426  
C:Genetics:  
A:Gene: GDB:SNAP  
A:Cross-references: GDB:355671; OMIM:600322  
A:Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 89; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 4  
I67823  
nerve terminal protein - human  
C:Species: Homo sapiens (man)  
C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Nov-1999  
C:Accession: I67823  
R:Bark, I.C.; Wilson, M.C.  
Gene 139, 291-292, 1994  
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein  
A:Reference number: I53735; MUID:94156217; PMID:8112622  
A:Accession: I67823  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-206 <RES>  
A:Cross-references: GB:L19761; NID:g307427; PIDN:AAC37546.1; PID:g307428  
C:Genetics:  
A:Gene: GDB:SNAP  
A:Cross-references: GDB:355671; OMIM:600322  
A:Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 89; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 5  
A33623  
synaptosomal-associated 25K protein - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 04-Apr-1990 #sequence\_revision 04-Apr-1990 #text\_change 05-Nov-1999  
C:Accession: A33623  
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.;  
J. Cell Biol. 109, 3039-3052, 1989  
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differ  
A:Reference number: A33623; MUID:90078337; PMID:2592413  
A:Accession: A33623  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-206 <OYL>  
A:Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998

Query Match 100.0%; Score 89; DB 2; Length 206;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 6  
I50481  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I50481  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MUID:94068448; PMID:8248151  
A:Accession: I50481  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-203 <RIS>  
A:Cross-references: GB:L22976; NID:g349430; PIDN:AAA16538.1; PID:g349431  
C:Genetics:  
A:Gene: SNAP-25

Query Match 89.9%; Score 80; DB 2; Length 203;  
Best Local Similarity 88.9%; Pred. No. 1.4e-05;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 177 RIMEKADSNKTRIDEANQ 194

RESULT 7  
I50552  
synapse protein - marbled electric ray  
C:Species: Torpedo marmorata (marbled electric ray)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I50552  
R:Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.  
J. Biol. Chem. 268, 24408-24414, 1993  
A:Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) s  
A:Reference number: A49513; MUID:94043281; PMID:8226991  
A:Accession: I50552  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-210 <RIS>  
A:Cross-references: GB:L22020; NID:g431296; PIDN:AAA49284.1; PID:g431297

Query Match 67.4%; Score 60; DB 2; Length 210;  
Best Local Similarity 66.7%; Pred. No. 0.026;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 187 RIVKGDINKARIDEANK 204

RESULT 8  
JC5512  
SNARE protein 23 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 05-Nov-1999  
C:Accession: JC5512  
R:Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Ok  
Biochem. Biophys. Res. Commun. 234, 257-262, 1997  
A:Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.  
A:Reference number: JC5512; MUID:97312558; PMID:9168999  
A:Accession: JC5512



A;Molecule type: mRNA  
A;Residues: 1-210 <ARA>  
A;Cross-references: DDBJ:G2189950; PIDN:BAA20345.1; PID:d1021177; PID:g218  
C;Comment: This protein is involved in the insulin-induced translocation of vesicles con

Query Match 66.3%; Score 59; DB 2; Length 210;  
Best Local Similarity 70.6%; Pred. No. 0.038;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17  
:|||||:|||||  
Db 185 KITEKADTNKTRIDIAN 201

## RESULT 9

JC5297  
vesicle-membrane fusion protein SNAP-23B - human  
C;Species: Homo sapiens (man)  
C;Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 05-Nov-1999  
C;Accession: JC5297  
R;Mollinedo, F.; Lazo, P.A.  
Biochem. Biophys. Res. Commun. 231, 808-812, 1997  
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23  
A;Reference number: JC5296; MUID:97224437; PMID:9070898  
A;Accession: JC5297

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA  
A;Residues: 1-158 <MOL>  
A;Cross-references: GB:Y09568; NID:g1924943; PIDN:CAA70761.1; PID:e290774; PID:g1924944  
A;Experimental source: neutrophils  
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cen

Query Match 61.8%; Score 55; DB 2; Length 158;  
Best Local Similarity 64.7%; Pred. No. 0.13;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17  
|||:||||:|||||  
Db 133 RITDKADTNRRDRIDIAN 149

## RESULT 10

JC5296  
vesicle-membrane fusion protein SNAP-23A - human  
C;Species: Homo sapiens (man)  
C;Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 05-Nov-1999  
C;Accession: JC5296  
R;Mollinedo, F.; Lazo, P.A.  
Biochem. Biophys. Res. Commun. 231, 808-812, 1997  
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23  
A;Reference number: JC5296; MUID:97224437; PMID:9070898  
A;Accession: JC5296

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA  
A;Residues: 1-211 <MOL>  
A;Cross-references: GB:Y09567; NID:g1924941; PIDN:CAA70760.1; PID:e290695; PID:g1924942  
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cen

Query Match 61.8%; Score 55; DB 2; Length 211;  
Best Local Similarity 64.7%; Pred. No. 0.17;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17  
|||:||||:|||||  
Db 186 RITDKADTNRRDRIDIAN 202

## RESULT 11

A49708  
synaptosomal-associated 25K protein - rat (fragments)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 12-Jun-1998  
C;Accession: A49708

R;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.;  
J. Biol. Chem. 269, 1617-1620, 1994

A;Title: Proteolysis of SNAP-25 by types E and A botulinum neurotoxins.

A;Reference number: A49708; MUID:94124495; PMID:8294407

A;Accession: A49708

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-29 <BIN>

Query Match 60.7%; Score 54; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IMEKADSNKTR 12  
|||||  
Db 11 IMEKADSNKTR 21

## RESULT 12

T26553  
hypothetical protein Y22F5A.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T26553  
R;Gardner, A.  
submitted to the EMBL Data Library, January 1998  
A;Reference number: Z20231  
A;Accession: T26553  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-234 <WIL>  
A;Cross-references: EMBL:AL021479; PIDN:CAA16322.1; GSPDB:GN00023; CESP:Y22F5A.3  
A;Experimental source: clone Y22F5A  
C;Genetics:  
A;Gene: CESP:Y22F5A.3  
A;Map position: 5  
A;Introns: 51/3; 82/1; 165/2; 213/3

Query Match 56.2%; Score 50; DB 2; Length 234;  
Best Local Similarity 50.0%; Pred. No. 1.2;  
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||:||||:|||||  
Db 209 RIHDKAQSNVRESANK 226

## RESULT 13

T24635  
hypothetical protein T07C4.10a - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 01-Dec-2000  
C;Accession: T24635; S41023  
R;Buck, D.  
submitted to the EMBL Data Library, February 1995  
A;Reference number: Z19915  
A;Accession: T24635  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: DNA  
A;Residues: 1-1138 <WIL>  
A;Cross-references: EMBL:Z48055; PIDN:CAA88136.1; GSPDB:GN00021; CESP:T07C4.10a  
A;Experimental source: clone T07A5  
R;Berks, M.  
submitted to the EMBL Data Library, January 1994  
A;Reference number: S41014  
A;Accession: S41023  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 895-1138 <BER>  
A;Cross-references: EMBL:Z29443  
C;Genetics:  
A;Gene: CESP:T07C4.10a  
A;Map position: 3

Search completed: March 9, 2004, 11:10:14  
Job time : 14.1351 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:07:42 ; Search time 26.7568 Seconds  
(without alignments)  
142.049 Million cell updates/sec

Title: US-10-030-485A-5  
Perfect score: 89  
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	33	10 US-09-942-024-33	Sequence 33, Appl
2	89	100.0	33	10 US-09-942-024-38	Sequence 38, Appl
3	89	100.0	33	10 US-09-942-098-33	Sequence 33, Appl
4	89	100.0	33	10 US-09-942-098-38	Sequence 38, Appl
5	89	100.0	116	10 US-09-962-360B-11	Sequence 11, Appl
6	89	100.0	116	10 US-09-962-360B-12	Sequence 12, Appl
7	89	100.0	206	10 US-09-942-024-2	Sequence 2, Appli
8	89	100.0	206	10 US-09-942-024-7	Sequence 7, Appli
9	89	100.0	206	10 US-09-942-024-12	Sequence 12, Appl
10	89	100.0	206	10 US-09-942-098-2	Sequence 2, Appli
11	89	100.0	206	10 US-09-942-098-7	Sequence 7, Appli
12	89	100.0	206	10 US-09-942-098-12	Sequence 12, Appl
13	80	89.9	33	10 US-09-942-024-37	Sequence 37, Appl
14	80	89.9	33	10 US-09-942-098-37	Sequence 37, Appl
15	80	89.9	203	10 US-09-942-024-14	Sequence 14, Appl

16	80	89.9	203	10 US-09-942-098-14	Sequence 14, Appl
17	65	73.0	21	10 US-09-942-024-89	Sequence 89, Appl
18	65	73.0	21	10 US-09-942-098-89	Sequence 89, Appl
19	65	73.0	24	10 US-09-942-024-90	Sequence 90, Appl
20	65	73.0	24	10 US-09-942-098-90	Sequence 90, Appl
21	61	68.5	13	10 US-09-942-024-86	Sequence 86, Appl
22	61	68.5	13	10 US-09-942-098-86	Sequence 86, Appl
23	61	68.5	17	10 US-09-942-024-31	Sequence 31, Appl
24	61	68.5	17	10 US-09-942-098-31	Sequence 31, Appl
25	61	68.5	18	10 US-09-942-024-32	Sequence 32, Appl
26	61	68.5	18	10 US-09-942-098-32	Sequence 32, Appl
27	61	68.5	23	10 US-09-942-024-88	Sequence 88, Appl
28	61	68.5	23	10 US-09-942-098-88	Sequence 88, Appl
29	60	67.4	30	10 US-09-942-024-39	Sequence 39, Appl
30	60	67.4	30	10 US-09-942-098-39	Sequence 39, Appl
31	59	66.3	32	10 US-09-942-024-35	Sequence 35, Appl
32	59	66.3	32	10 US-09-942-098-35	Sequence 35, Appl
33	55	61.8	15	10 US-09-942-024-28	Sequence 28, Appl
34	55	61.8	15	10 US-09-942-098-28	Sequence 28, Appl
35	55	61.8	16	10 US-09-942-024-29	Sequence 29, Appl
36	55	61.8	16	10 US-09-942-098-29	Sequence 29, Appl
37	55	61.8	17	10 US-09-942-024-30	Sequence 30, Appl
38	55	61.8	17	10 US-09-942-024-44	Sequence 44, Appl
39	55	61.8	17	10 US-09-942-024-45	Sequence 45, Appl
40	55	61.8	17	10 US-09-942-024-46	Sequence 46, Appl
41	55	61.8	17	10 US-09-942-024-47	Sequence 47, Appl
42	55	61.8	17	10 US-09-942-024-48	Sequence 48, Appl
43	55	61.8	17	10 US-09-942-024-49	Sequence 49, Appl
44	55	61.8	17	10 US-09-942-098-30	Sequence 30, Appl
45	55	61.8	17	10 US-09-942-098-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1  
US-09-942-024-33  
; Sequence 33, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942, 024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-942-024-33

Query Match 100.0%; Score 89; DB 10; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||

Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 2  
US-09-942-024-38  
; Sequence 38, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-024-38

Query Match 100.0%; Score 89; DB 10; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 3  
US-09-942-098-33  
; Sequence 33, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; TITLE OF INVENTION: Toxins  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-942-098-33

Query Match 100.0%; Score 89; DB 10; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 4  
US-09-942-098-38  
; Sequence 38, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; TITLE OF INVENTION: Toxins  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-098-38

Query Match 100.0%; Score 89; DB 10; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 5  
US-09-962-360B-11  
; Sequence 11, Application US/09962360B  
; Publication No. US20030077685A1  
; GENERAL INFORMATION:  
; /9  
; APPLICANT: Schmidt, James J.  
; APPLICANT: Stafford, Robert G.  
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostric  
; TITLE OF INVENTION: Neurotoxins  
; FILE REFERENCE: 003/224/SAP  
; CURRENT APPLICATION NUMBER: US/09/962,360B  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/235,050  
; PRIOR FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 11  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1  
; OTHER INFORMATION: Xaa at 1 is S-fluorenceinyl-cysteine  
US-09-962-360B-11

Query Match 100.0%; Score 89; DB 10; Length 116;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 89 RIMEKADSNKTRIDEANQ 106

RESULT 6  
US-09-962-360B-12  
; Sequence 12, Application US/09962360B  
; Publication No. US20030077685A1  
; GENERAL INFORMATION:  
; /9  
; APPLICANT: Schmidt, James J.  
; APPLICANT: Stafford, Robert G.  
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostric  
; TITLE OF INVENTION: Neurotoxins  
; FILE REFERENCE: 003/224/SAP  
; CURRENT APPLICATION NUMBER: US/09/962,360B  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/235,050  
; PRIOR FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 12  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1

; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine  
US-09-962-360B-12

Query Match 100.0%; Score 89; DB 10; Length 116;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 89 RIMEKADSNKTRIDEANQ 106

## RESULT 7

US-09-942-024-2  
; Sequence 2, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:

; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: Serotype A/E Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-942-024-2

Query Match 100.0%; Score 89; DB 10; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

## RESULT 8

US-09-942-024-7  
; Sequence 7, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:

; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: Serotype A/E Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Rattus sp.

US-09-942-024-7

Query Match 100.0%; Score 89; DB 10; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

## RESULT 9

US-09-942-024-12  
; Sequence 12, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:

; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: Serotype A/E Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Mus musculus

US-09-942-024-12

Query Match 100.0%; Score 89; DB 10; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

## RESULT 10

US-09-942-098-2  
; Sequence 2, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:

; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; FILE REFERENCE: Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-942-098-2

Query Match 100.0%; Score 89; DB 10; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||  
Db 180 RIMEKADSNKTRIDEANQ 197

## RESULT 11

US-09-942-098-7  
; Sequence 7, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:

; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; FILE REFERENCE: Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-942-098-7

Query Match 100.0%; Score 89; DB 10; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||: |||||  
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 12  
US-09-942-098-12  
; Sequence 12, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; TITLE OF INVENTION: Toxins  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-942-098-12

Query Match 100.0%; Score 89; DB 10; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||: |||||  
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 13  
US-09-942-024-37  
; Sequence 37, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-024-37

Query Match 89.9%; Score 80; DB 10; Length 33;  
Best Local Similarity 88.9%; Pred. No. 3.6e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||: |||||

Db 7 RIMDMADSNKTRIDEANQ 24

RESULT 14  
US-09-942-098-37  
; Sequence 37, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; TITLE OF INVENTION: Toxins  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-098-37

Query Match 89.9%; Score 80; DB 10; Length 33;  
Best Local Similarity 88.9%; Pred. No. 3.6e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||: |||||  
Db 7 RIMDMADSNKTRIDEANQ 24

RESULT 15  
US-09-942-024-14  
; Sequence 14, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Carassius auratus  
US-09-942-024-14

Query Match 89.9%; Score 80; DB 10; Length 203;  
Best Local Similarity 88.9%; Pred. No. 2.9e-05;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||: |||||  
Db 177 RIMDMADSNKTRIDEANQ 194

Search completed: March 9, 2004, 11:12:07  
Job time : 27.7568 secs



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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:05:46 ; Search time 16.0541 Seconds  
(without alignments)  
57.884 Million cell updates/sec

Title: US-10-030-485A-5  
Perfect score: 89  
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	89	100.0	37	3	US-08-819-286-4
2	89	100.0	70	2	US-08-760-001-10
3	89	100.0	70	3	US-09-015-960-10
4	89	100.0	70	4	US-09-534-572-10
5	89	100.0	206	1	US-08-393-985-18
6	89	100.0	206	3	US-08-819-286-1
7	84	94.4	26	3	US-08-819-286-8
8	55	61.8	15	2	US-08-743-894B-38
9	55	61.8	16	2	US-08-743-894B-49
10	55	61.8	17	2	US-08-743-894B-1
11	55	61.8	17	2	US-08-743-894B-24
12	55	61.8	17	2	US-08-743-894B-25
13	55	61.8	17	2	US-08-743-894B-26
14	55	61.8	17	2	US-08-743-894B-27
15	55	61.8	17	2	US-08-743-894B-28
16	55	61.8	17	2	US-08-743-894B-31
17	55	61.8	17	2	US-08-743-894B-32
18	55	61.8	17	2	US-08-743-894B-37
19	55	61.8	17	2	US-08-743-894B-39
20	55	61.8	17	2	US-08-743-894B-42
21	55	61.8	17	2	US-08-743-894B-43
22	55	61.8	17	2	US-08-743-894B-44
23	55	61.8	17	2	US-08-743-894B-45
24	55	61.8	17	2	US-08-743-894B-47
25	55	61.8	20	3	US-08-819-286-9
26	52	58.4	16	2	US-08-743-894B-51
27	52	58.4	16	2	US-08-743-894B-52

28	52	58.4	16	2	US-08-743-894B-54
29	52	58.4	17	2	US-08-743-894B-2
30	52	58.4	17	2	US-08-743-894B-5
31	52	58.4	17	2	US-08-743-894B-6
32	52	58.4	17	2	US-08-743-894B-18
33	51	57.3	17	2	US-08-743-894B-30
34	50	56.2	17	2	US-08-743-894B-19
35	50	56.2	17	2	US-08-743-894B-29
36	50	56.2	17	2	US-08-743-894B-33
37	50	56.2	17	2	US-08-743-894B-34
38	50	56.2	17	2	US-08-743-894B-48
39	50	56.2	17	2	US-08-743-894B-50
40	49	55.1	16	2	US-08-743-894B-12
41	49	55.1	16	3	US-08-819-286-12
42	49	55.1	17	2	US-08-743-894B-3
43	49	55.1	17	2	US-08-743-894B-20
44	49	55.1	17	2	US-08-743-894B-36
45	49	55.1	17	2	US-08-743-894B-46

ALIGNMENTS

RESULT 1  
US-08-819-286-4  
; Sequence 4, Application US/08819286  
; Patent No. 6169074  
; GENERAL INFORMATION:  
; APPLICANT: Montal, Mauricio  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF  
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/819,286  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,599  
; FILING DATE: 18-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Taylor, Stacy L.  
; REGISTRATION NUMBER: 34,842  
; REFERENCE/DOCKET NUMBER: 07349/005001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-819-286-4

Query Match 100.0%; Score 89; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
|||||

Db 11 RIMEKADSNKTRIDEANQ 28

## RESULT 2

US-08-760-001-10  
; Sequence 10, Application US/08760001  
; Patent No. 5962637  
; GENERAL INFORMATION:  
; APPLICANT: Shone, Clifford C.  
; APPLICANT: Hallis, Bassam  
; APPLICANT: James, Benjamin A. F.  
; APPLICANT: Quinn, Conrad P.  
; TITLE OF INVENTION: TOXIN ASSAY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,001  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/01279  
; FILING DATE: 02-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1581.0120001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2543  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 70 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-760-001-10

Query Match 100.0%; Score 89; DB 2; Length 70;  
Best Local Similarity 100.0%; Pred. No. 3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
Db 44 RIMEKADSNKTRIDEANQ 61

## RESULT 3

US-09-015-960-10  
; Sequence 10, Application US/09015960  
; Patent No. 6043042  
; GENERAL INFORMATION:  
; APPLICANT: Shone, Clifford C.  
; APPLICANT: Hallis, Bassam  
; APPLICANT: James, Benjamin A. F.  
; APPLICANT: Quinn, Conrad P.  
; TITLE OF INVENTION: TOXIN ASSAY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington

; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/015,960  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/760,001  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1581.0120001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2543  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 70 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-015-960-10

Query Match 100.0%; Score 89; DB 3; Length 70;  
Best Local Similarity 100.0%; Pred. No. 3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
Db 44 RIMEKADSNKTRIDEANQ 61

## RESULT 4

US-09-534-572-10  
; Sequence 10, Application US/09534572  
; Patent No. 6337386  
; GENERAL INFORMATION:  
; APPLICANT: Shone, Clifford C.  
; APPLICANT: Hallis, Bassam  
; APPLICANT: James, Benjamin A. F.  
; APPLICANT: Quinn, Conrad P.  
; TITLE OF INVENTION: TOXIN ASSAY  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/534,572  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/015,960  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/760,001  
; FILING DATE: 30-DEC-1996

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/GB95/01279  
;; FILING DATE: 02-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Emond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 1581.0120003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2543  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 70 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-09-534-572-10

Query Match 100.0%; Score 89; DB 4; Length 70;  
Best Local Similarity 100.0%; Pred. No. 3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
Db 44 RIMEKADSNKTRIDEANQ 61

RESULT 5  
US-08-393-985-18  
; Sequence 18, Application US/08393985  
; Patent No. 5693476  
; GENERAL INFORMATION:  
; APPLICANT: Scheller, Richard H.  
; TITLE OF INVENTION: Methods and Compositions for Modulation  
; TITLE OF INVENTION: of Vesicular Release  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/393,985  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sholtz, Charles K.  
;; REGISTRATION NUMBER: 38,615  
;; REFERENCE/DOCKET NUMBER: 8600-0152  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 324-0880  
;; TELEFAX: (415) 324-0960  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 206 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-393-985-18

Query Match 100.0%; Score 89; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18

Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 6  
US-08-819-286-1  
; Sequence 1, Application US/08819286  
; Patent No. 6169074  
; GENERAL INFORMATION:  
; APPLICANT: Montal, Mauricio  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF  
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/819,286  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/013,599  
;; FILING DATE: 18-MAR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Taylor, Stacy L.  
;; REGISTRATION NUMBER: 34,842  
;; REFERENCE/DOCKET NUMBER: 07349/005001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619/678-5070  
;; TELEFAX: 619/678-5099  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 206 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-819-286-1

Query Match 100.0%; Score 89; DB 3; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18  
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 7  
US-08-819-286-8  
; Sequence 8, Application US/08819286  
; Patent No. 6169074  
; GENERAL INFORMATION:  
; APPLICANT: Montal, Mauricio  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF  
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/819,286  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,599  
; FILING DATE: 18-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Taylor, Stacy L.  
; REGISTRATION NUMBER: 34,842  
; REFERENCE/DOCKET NUMBER: 07349/005001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-819-286-8

Query Match 94.4%; Score 84; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 6.8e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IMEKADSNKTRIDEANQ 18  
Db 1 IMEKADSNKTRIDEANQ 17

## RESULT 8

US-08-743-894B-38  
; Sequence 38, Application US/08743894B  
; Patent No. 5965699  
; GENERAL INFORMATION:  
; APPLICANT: James J. Schmidt  
; APPLICANT: Karen A. Bostian  
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty  
; STREET: USA MPMC - 504 Scott Street  
; CITY: FORT DETRICK  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 21702-5012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.0  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/743,894B  
; FILING DATE: No. 5965699ember 6, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Charles H. Harris  
; REGISTRATION NUMBER: 34,616  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 619-2065  
; TELEFAX: (301) 619-7714  
; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid sequence  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; FEATURE:  
; US-08-743-894B-38

Query Match 61.8%; Score 55; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SNKTRIDEANQ 18  
Db 1 SNKTRIDEANQ 11

## RESULT 9

US-08-743-894B-49  
; Sequence 49, Application US/08743894B  
; Patent No. 5965699  
; GENERAL INFORMATION:  
; APPLICANT: James J. Schmidt  
; APPLICANT: Karen A. Bostian  
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty  
; STREET: USA MPMC - 504 Scott Street  
; CITY: FORT DETRICK  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 21702-5012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.0  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/743,894B  
; FILING DATE: No. 5965699ember 6, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Charles H. Harris  
; REGISTRATION NUMBER: 34,616  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 619-2065  
; TELEFAX: (301) 619-7714  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid sequence  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; FEATURE:  
; US-08-743-894B-49

Query Match 61.8%; Score 55; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SNKTRIDEANQ 18  
Db 1 SNKTRIDEANQ 11

## RESULT 10

US-08-743-894B-1  
; Sequence 1, Application US/08743894B

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; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-743-894B-1
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; Query Match 61.8%; Score 55; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 0.0037;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 8 SNKTRIDEANQ 18
; Db 1 SNKTRIDEANQ 11
;
; RESULT 11
; US-08-743-894B-24
; Sequence 24, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-25
;
; Query Match 61.8%; Score 55; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 0.0037;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 8 SNKTRIDEANQ 18
; Db 1 SNKTRIDEANQ 11
;
; RESULT 12
; US-08-743-894B-25
; Sequence 25, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-24
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 16
; OTHER INFORMATION: Xaa represents norleucine
; US-08-743-894B-24
;
; Query Match 61.8%; Score 55; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 0.0037;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 8 SNKTRIDEANQ 18
; Db 1 SNKTRIDEANQ 11
;
; RESULT 12
; US-08-743-894B-25
; Sequence 25, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-24
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; LOCATION: 14
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-25

Query Match      61.8%; Score 55; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 SNKTRIDEANQ 18
      |||||
Db      1 SNKTRIDEANQ 11

RESULT 13
US-08-743-894B-26
; Sequence 26, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-27

Query Match      61.8%; Score 55; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 SNKTRIDEANQ 18
      |||||
Db      1 SNKTRIDEANQ 11

RESULT 15
US-08-743-894B-28
; Sequence 28, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-26

Query Match      61.8%; Score 55; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 SNKTRIDEANQ 18
      |||||
Db      1 SNKTRIDEANQ 11

RESULT 14
US-08-743-894B-27
; Sequence 27, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
```



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-28

Query Match 61.8%; Score 55; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SNKTRIDEANQ 18
Db 1 SNKTRIDEANQ 11
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Search completed: March 9, 2004, 11:10:59  
Job time : 16.0541 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: March 9, 2004, 10:57:21 ; Search time 49.6216 Seconds  
(without alignments)  
102.493 Million cell updates/sec

Title: US-10-030-485A-5  
Perfect score: 89  
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	18	AAB15585	Aab15585 Human SNA
2	89	100.0	33	AAE36683	Aae36683 Goldfish
3	89	100.0	33	AAE36678	Aae36678 SNAP-25 p
4	89	100.0	37	AAW30097	Aaw30097 Neurotran
5	89	100.0	70	AAR86823	Aar86823 SNAP-25 r
6	89	100.0	86	AAB15584	Aab15584 Human SNA
7	89	100.0	116	AAO15165	Aao15165 Clostridi
8	89	100.0	116	AAO15166	Aao15166 Clostridi
9	89	100.0	198	AAU00255	Aau00255 Synaptoso
10	89	100.0	199	AAU00263	Aau00263 Synaptoso
11	89	100.0	200	AAU00264	Aau00264 Synaptoso
12	89	100.0	201	AAU00267	Aau00267 Synaptoso
13	89	100.0	202	AAU00265	Aau00265 Synaptoso
14	89	100.0	203	AAU002636	Aau002636 Synaptoso
15	89	100.0	206	AAW30103	Aaw30103 Synaptoso
16	89	100.0	206	AAW43426	Aaw43426 Mouse syn
17	89	100.0	206	AAW79198	Aaw79198 Mouse SNA
18	89	100.0	206	AAU00261	Aau00261 Synaptoso
19	89	100.0	206	AAU00246	Aau00246 Synaptoso
20	89	100.0	206	AAU00253	Aau00253 SNARE hom
21	89	100.0	206	AAU02171	Aau02171 Synaptoso
22	89	100.0	206	AAU02640	Aau02640 Synaptoso
23	89	100.0	206	AAU00259	Aau00259 Synaptoso
24	89	100.0	206	AAU00252	Aau00252 SNARE hom
25	89	100.0	206	AAU02638	Aau02638 Synaptoso

26	89	100.0	206	4	AAU02639	Synaptoso
27	89	100.0	206	6	AAE36662	Human SNA
28	89	100.0	206	6	AAE36667	Rat VAMP-
29	89	100.0	206	7	ADE54280	Rat Prote
30	89	100.0	206	7	ADE54288	Rat Prote
31	89	100.0	206	7	ADE54276	Rat Prote
32	89	100.0	206	7	ADE54290	Human Pro
33	89	100.0	206	7	ADE54282	Rat Prote
34	89	100.0	206	7	ADE54274	Rat Prote
35	89	100.0	206	7	ADE54286	Human Pro
36	89	100.0	206	7	ADE54284	Rat Prote
37	89	100.0	206	7	ADE54272	Rat Prote
38	89	100.0	206	7	ADE54278	Rat Prote
39	85	95.5	206	4	AAU00266	Synaptoso
40	85	95.5	206	4	AAU00262	Synaptoso
41	84	94.4	26	2	AAW30099	Neurotran
42	84	94.4	206	4	AAU00256	Synaptoso
43	84	94.4	206	4	AAU00258	Synaptoso
44	84	94.4	206	4	AAU00260	Synaptoso
45	84	94.4	206	4	AAU00257	Synaptoso

ALIGNMENTS

RESULT 1  
AAB15585  
ID AAB15585 standard; peptide; 18 AA.  
XX AAB15585;  
AC  
XX 02-MAR-2001 (first entry)  
DT  
XX Human SNAP-25 N-terminal peptide #5.  
DE  
XX Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;  
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;  
KW neurodegenerative disorder.  
XX Homo sapiens.  
OS  
XX WO200064932-A1.  
PN  
XX 02-NOV-2000.  
PD  
XX 18-FEB-2000; 2000WO-ES000058.  
PF  
XX 23-APR-1999; 99ES-00000844.  
PR (LIPO-) LIPOTEC SA.  
XX  
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;  
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;  
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;  
PI Perez Paya E;  
XX  
XX WPI; 2001-007091/01.  
XX  
XX New peptides containing amino acid sequences from known proteins for  
treatment of neurological disorders.  
PT  
XX Claim 17; Page 33; 40pp; Spanish.  
XX  
XX The invention relates to new peptides comprising 3-30 contiguous amino  
acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated  
protein 25). The peptides AAB15581-B15586 represent examples of the  
peptides of the invention. The peptides have neuronal exocytosis  
inhibitory activity and are used for treatment of facial wrinkles and  
asymmetry and pathological neuronal exocytosis-mediated pathological  
disorders and alterations manifested e.g. by spasms and neurological and  
neurodegenerative disorders  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 89; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
Db 1 RIMEKADSNKTRIDEANQ 18

RESULT 2  
AAE36683  
ID AAE36683 standard; peptide; 33 AA.  
XX AAE36683;  
AC AAE36683;  
XX 07-AUG-2003 (first entry)  
XX Goldfish SNAP-25B peptide.  
DE Goldfish SNAP-25B peptide.  
XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;  
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;  
KW TeNT; cosmetic.  
XX Carassius auratus.  
OS Key Location/Qualifiers  
XX Cleavage-site 7. .8 /note= "BoNT/E sensitive cleavage site"  
FH Cleavage-site 24. .25 /note= "BoNT/A sensitive cleavage site"  
FT Cleavage-site 25. .26 /note= "BoNT/C sensitive cleavage site"  
FT WO2003020948-A2.  
XX 13-MAR-2003.  
PD 22-AUG-2002; 2002WO-US027145.  
XX 28-AUG-2001; 2001US-00942024.  
PR (ALLR ) ALLERGAN INC.  
XX Steward LE, Fernandez-Salas E, Aoki KR;  
XX WPI; 2003-290198/28.  
XX Botulinum serotype A/E substrate useful for assaying protease activity of  
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial  
PT toxin recognition sequence that includes a cleavage site.  
XX Disclosure; Page 42; 168pp; English.  
XX The present invention relates to novel clostridium toxin substrates. The  
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates  
CC which comprise a donor fluorophore, an acceptor having an absorbance  
CC spectrum overlapping the emission spectrum of the donor fluorophore and a  
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where  
CC the cleavage site intervenes between the donor fluorophore and acceptor  
CC and under the appropriate conditions, the resonance energy transfer is  
CC exhibited between the donor and acceptor. Natural targets of clostridium  
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences  
CC of the invention are useful in assaying for the protease activity of any  
CC clostridial toxin including botulinum toxins of all serotypes and tetanus  
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast  
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil  
CC samples, water samples, cosmetics, tissue samples and beverage or food  
CC samples. They are useful to assay a sample from a human or animal, for  
CC e.g., exposed to clostridial toxin or having one or more symptoms of a  
CC clostridial toxin, to follow activity during production and purification  
CC of clostridial toxin and to assay formulated clostridial toxin products  
CC including pharmaceuticals and cosmetics. The present sequence is goldfish

CC SNAP-25B peptide used in the invention  
XX Sequence 33 AA;  
SQ Query Match 100.0%; Score 89; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 3  
AAE36678  
ID AAE36678 standard; peptide; 33 AA.  
XX AAE36678;  
AC AAE36678;  
XX 07-AUG-2003 (first entry)  
XX SNAP-25 peptide.  
DE Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;  
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;  
KW cosmetic; mouse; rat.  
XX Homo sapiens.  
OS Mus musculus.  
OS Rattus sp.  
XX Key Location/Qualifiers  
FH Cleavage-site 7. .8 /note= "BoNT/E sensitive cleavage site"  
FT Cleavage-site 24. .25 /note= "BoNT/A sensitive cleavage site"  
FT Cleavage-site 25. .26 /note= "BoNT/C sensitive cleavage site"  
FT WO2003020948-A2.  
XX 13-MAR-2003.  
PD 22-AUG-2002; 2002WO-US027145.  
XX 28-AUG-2001; 2001US-00942024.  
PR (ALLR ) ALLERGAN INC.  
XX Steward LE, Fernandez-Salas E, Aoki KR;  
XX WPI; 2003-290198/28.  
XX Botulinum serotype A/E substrate useful for assaying protease activity of  
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial  
PT toxin recognition sequence that includes a cleavage site.  
XX Disclosure; Page 42; 168pp; English.  
XX The present invention relates to novel clostridium toxin substrates. The  
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates  
CC which comprise a donor fluorophore, an acceptor having an absorbance  
CC spectrum overlapping the emission spectrum of the donor fluorophore and a  
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where  
CC the cleavage site intervenes between the donor fluorophore and acceptor  
CC and under the appropriate conditions, the resonance energy transfer is  
CC exhibited between the donor and acceptor. Natural targets of clostridium  
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences  
CC of the invention are useful in assaying for the protease activity of any  
CC clostridial toxin including botulinum toxins of all serotypes and tetanus  
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast  
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil  
CC samples, water samples, cosmetics, tissue samples and beverage or food

CC samples. They are useful to assay a sample from a human or animal, for  
CC e.g., exposed to clostridial toxin or having one or more symptoms of a  
CC clostridial toxin, to follow activity during production and purification  
CC of clostridial toxin and to assay formulated clostridial toxin products  
CC including pharmaceuticals and cosmetics. The present sequence is SNAP-25  
CC peptide used in the invention  
XX  
SQ Sequence 33 AA;

Query Match 100.0%; Score 89; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIMEKADSNKTRIDEANQ 18  
Db 7 RIMEKADSNKTRIDEANQ 24  
|||||

RESULT 4  
AAW30097  
ID AAW30097 standard; peptide; 37 AA.  
XX  
AC AAW30097;

DT 06-APR-1998 (first entry)  
XX Neurotransmitter secretion inhibitor #1.

DE Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;  
XX excitation-secretory uncoupling peptide; catecholamine secretion;  
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
KW synaptosomal associated protein; SNAP-25.

XX Homo sapiens.  
OS  
XX WO9734620-A1.  
PN  
XX 25-SEP-1997.

PF 18-MAR-1997; 97WO-US004393.

PR 18-MAR-1996; 96US-0013599P.

XX (REGC ) UNIV CALIFORNIA.

XX Montal M;

XX WPI; 1997-479986/44.

XX Excitation-secretory uncoupling peptide(s) for inhibiting  
PT neurotransmitter release - used particularly for treating muscle  
PT spasticity, and for delivering drugs specifically to neural cells.

XX Claim 1; Page 30; 61pp; English.

CC This sequence corresponds to residues 170-206 of the human 25 kD  
CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of  
CC the invention. The agents of the invention inhibit secretion of  
CC neurotransmitter from neuronal cells and is an excitation-secretory  
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which  
CC correspond substantially to any one of AAW30097-W30102, or more generally  
CC any (I) that inhibits 50% of catecholamine secretion from bovine  
CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,  
CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit  
CC release of neurotransmitters from synaptic vesicles, specifically for  
CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo  
CC imaging of intracellular distribution of (I). Compounds for delivering  
CC the drug to neural cells provide targeted drug delivery, e.g. of  
CC substance P to brain tumours for induction of apoptosis. Unlike the  
CC neurotoxins, (I) are not toxic or immunogenic and are more readily  
CC available. Their therapeutic effect lasts for several days or weeks, so  
CC lower doses or less frequent treatments are required  
XX

SQ Sequence 37 AA;

Query Match 100.0%; Score 89; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIMEKADSNKTRIDEANQ 18  
Db 11 RIMEKADSNKTRIDEANQ 28  
|||||

RESULT 5  
AAR86823  
ID AAR86823 standard; peptide; 70 AA.

XX  
AC AAR86823;

DT 15-AUG-1996 (first entry)

XX SNAP-25 residues 137-206.

XX VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;  
KW neurotransmitter; neurotoxin; botulinum; cleavage; substrate;  
KW antibody; detection; assay.

XX Synthetic.

XX WO9533850-A1.

XX 14-DEC-1995.

XX 02-JUN-1995; 95WO-GB001279.

XX 03-JUN-1994; 94GB-00011138.

XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.

XX Shone CC, Hallis B, James BAF, Quinn CP;

XX WPI; 1996-040249/04.

XX Assay for botulinum or tetanus toxin - by combining test cpd. with  
PT substrate which is cleaved by the toxin, and antibody specific for the  
PT cleaved but not uncleaved substrate.

XX Example 4; Page 19; 48pp; English.

XX The botulinum neurotoxins possess highly specific zinc-endopeptidase  
CC activities within their light sub-units. Depending on the neurotoxin type  
CC these act to cleave small proteins within the nerve cell which are  
CC involved in neurotransmitter release. Antibodies are used in assays which  
CC detect cleaved but not uncleaved substrate. Assays for botulinum types A  
CC and E use the present sequence as a substrate. The sequence is SNAP-25  
CC protein, residues 137-206

SQ Sequence 70 AA;

Query Match 100.0%; Score 89; DB 2; Length 70;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIMEKADSNKTRIDEANQ 18  
Db 44 RIMEKADSNKTRIDEANQ 61  
|||||

RESULT 6  
AAB15584  
ID AAB15584 standard; peptide; 86 AA.

XX  
AC AAB15584;

DT 02-MAR-2001 (first entry)  
XX Human SNAP-25 N-terminal peptide #4.  
DE Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;  
XX SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;  
KW neurodegenerative disorder.  
KW Homo sapiens.  
XX WO200064932-A1.  
XX 02-NOV-2000.  
PD 18-FEB-2000; 2000WO-ES000058.  
XX 23-APR-1999; 99ES-00000844.  
XX (LIPO-) LIPOTEC SA.  
XX Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;  
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;  
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;  
PI Perez Paya E;  
XX WPI; 2001-007091/01.  
DR New peptides containing amino acid sequences from known proteins for  
XX treatment of neurological disorders.  
XX Claim 16; Page 32-33; 40pp; Spanish.  
XX The invention relates to new peptides comprising 3-30 contiguous amino  
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated  
CC protein 25). The peptides AAB15581-B15586 represent examples of the  
CC peptides of the invention. The peptides have neuronal exocytosis  
CC inhibitory activity and are used for treatment of facial wrinkles and  
CC asymmetry and pathological neuronal exocytosis-mediated pathological  
CC disorders and alterations manifested e.g. by spasms and neurological and  
CC neurodegenerative disorders  
XX Sequence 86 AA;  
SQ  
Query Match 100.0%; Score 89; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RIMEKADSNKTRIDEANQ 18  
DB 60 RIMEKADSNKTRIDEANQ 77  
RESULT 7  
AAO15165  
ID AAO15165 standard; peptide; 116 AA.  
AC AAO15165;  
XX 02-SEP-2002 (first entry)  
DT Clostridial neurotoxin protease substrate peptide 4.  
DE Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;  
XX fluorescence resonant energy transfer assay; quenched-signal;  
KW clostridial neurotoxin detection; food.  
XX Unidentified.  
OS Key Location/Qualifiers  
XX Modified-site 1 /note= "S-fluoresceinyl-cysteine"  
FT Cleavage-site 89. .90  
FT /note= "The peptide is cleaved between these two residues  
FT

FT by type E Clostridium botulinum neurotoxin"  
FT Cleavage-site 106. .107  
FT /note= "The peptide is cleaved between these two residues  
FT by type A Clostridium botulinum neurotoxin"  
XX WO200225284-A2.  
PN 28-MAR-2002.  
XX 25-SEP-2001; 2001WO-US030188.  
XX 25-SEP-2000; 2000US-0235050P.  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
PA Schmidt JJ, Stafford RG;  
PI WPI; 2002-499829/53.  
XX Substrate useful in e.g. an assay for the protease activity of  
PT clostridial neurotoxin, comprises modified peptide or protein.  
XX Claim 22; Page 16; 48pp; English.  
XX The invention comprises clostridial neurotoxin substrate peptides which  
CC can serve as fluorescence resonant energy transfer assay (FRET) or  
CC quenched-signal substrates in assays for the proteolytic activities of  
CC clostridial neurotoxins. The invention further comprises Clostridium  
CC botulinum neurotoxin substrate peptides that can serve as immobilised  
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic  
CC activities of clostridial neurotoxins. The clostridial (including the  
CC Clostridium botulinum) neurotoxin substrate peptides are useful for  
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food  
CC or an environmental sample). The present amino acid sequence represents a  
CC clostridial neurotoxin substrate peptide of the invention  
SQ Sequence 116 AA;  
Query Match 100.0%; Score 89; DB 5; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RIMEKADSNKTRIDEANQ 18  
DB 89 RIMEKADSNKTRIDEANQ 106  
RESULT 8  
AAO15166  
ID AAO15166 standard; peptide; 116 AA.  
XX AAO15166;  
AC 02-SEP-2002 (first entry)  
DT Clostridial neurotoxin protease substrate peptide 5.  
DE Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;  
KW fluorescence resonant energy transfer assay; quenched-signal;  
KW clostridial neurotoxin detection; food.  
XX Unidentified.  
OS Key Location/Qualifiers  
XX Modified-site 1 /note= "S-fluoresceinyl-cysteine"  
FT Cleavage-site 89. .90  
FT /note= "The peptide is cleaved between these two residues  
FT by type E Clostridium botulinum neurotoxin"  
XX WO200225284-A2.  
PN 28-MAR-2002.  
PD

XX 25-SEP-2001; 2001WO-US030188.  
PF XX  
XX 25-SEP-2000; 2000US-0235050P.  
PR XX  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
PA  
PI Schmidt JJ, Stafford RG;  
XX WPI; 2002-499829/53.  
DR  
XX Substrate useful in e.g. an assay for the protease activity of  
PT clostridial neurotoxin, comprises modified peptide or protein.  
PT  
XX Claim 28; Page 17; 48pp; English.  
XX  
CC The invention comprises clostridial neurotoxin substrate peptides which  
CC can serve as fluorescence resonant energy transfer assay (FRET) or  
CC quenched-signal substrates in assays for the proteolytic activities of  
CC clostridial neurotoxins. The invention further comprises Clostridium  
CC botulinum neurotoxin substrate peptides that can serve as immobilised  
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic  
CC activities of clostridial neurotoxins. The clostridial (including the  
CC Clostridium botulinum) neurotoxin substrate peptides are useful for  
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food  
CC or an environmental sample). The present amino acid sequence represents a  
CC clostridial neurotoxin substrate peptide of the invention  
XX  
SQ Sequence 116 AA;  
  
Query Match 100.0%; Score 89; DB 5; Length 116;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RIMEKADSNKTRIDEANQ 18  
Db 89 RIMEKADSNKTRIDEANQ 106  
  
RESULT 9  
AAU00255  
ID AAU00255 standard; protein; 198 AA.  
XX  
AC AAU00255;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.  
XX  
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
KW synaptosomal-associated protein; mouse; mutant; mutein;  
KW N-ethylmaleimide-sensitive fusion protein;  
KW soluble NSF-attachment protein receptor.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
XX WO200118038-A2.  
XX  
PD 15-MAR-2001.  
XX  
PF 18-AUG-2000; 2000WO-GB003196.  
XX  
PR 20-AUG-1999; 99US-0149993P.  
XX  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
PI  
XX WPI; 2001-226739/23.  
DR  
XX Treating a patient suffering from poisoning or at risk of poisoning by a

PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
PT resistant or toxin-inhibitory SNARE.  
XX  
XX Example 1; Page; 131pp; English.  
XX  
CC The sequence represents the amino acid sequence of synaptosomal-  
CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new  
CC method of treating a patient suffering from poisoning or at risk of  
CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
CC useful in the manufacture of a medicament for the treatment of a patient  
CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
CC polynucleotide encoding either of these SNARE polypeptides are useful in  
CC the manufacture of medicament for the treatment of a patient in need of  
CC inhibition of SNARE-dependent exocytosis from a cell capable of  
CC performing SNARE-dependent exocytosis. The method of treatment is  
CC relatively fast, thus alleviating the symptoms when most severe and  
CC taking the patient out of critical state. Note: The present sequence is  
CC not shown in the specification but is derived from the mouse SNAP-25  
CC sequence given in figure 8 (see AAU00246)  
XX  
SQ Sequence 198 AA;  
  
Query Match 100.0%; Score 89; DB 4; Length 198;  
Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RIMEKADSNKTRIDEANQ 18  
Db 180 RIMEKADSNKTRIDEANQ 197  
  
RESULT 10  
AAU00263  
ID AAU00263 standard; protein; 199 AA.  
XX  
AC AAU00263;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Synaptosomal-associated protein, SNAP25, mutant 1-199(R198T).  
XX  
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
KW synaptosomal-associated protein; mouse; mutant; mutein;  
KW N-ethylmaleimide-sensitive fusion protein;  
KW soluble NSF-attachment protein receptor.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"  
FT  
XX  
XX WO200118038-A2.  
XX  
XX 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-GB003196.  
XX  
XX 20-AUG-1999; 99US-0149993P.  
XX



PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
 XX  
 DR WPI; 2001-226739/23.  
 XX  
 XX Treating a patient suffering from poisoning or at risk of poisoning by a  
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
 PT resistant or toxin-inhibitory SNARE.  
 XX  
 PS Example 1; Page; 131pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant 1-199(R198T), used in a new method of  
 CC treating a patient suffering from poisoning or at risk of poisoning by a  
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-  
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the  
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating  
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a  
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
 CC or a recombinant polynucleotide encoding the SNARE is useful in the  
 CC manufacture of a medicament for the treatment of a patient suffering from  
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from  
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a  
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
 CC either of these SNARE polypeptides are useful in the manufacture of  
 CC medicament for the treatment of a patient in need of inhibition of SNARE-  
 CC dependent exocytosis from a cell capable of performing SNARE-dependent  
 CC exocytosis. The method of treatment is relatively fast, thus alleviating  
 CC the symptoms when most severe and taking the patient out of critical  
 CC state. Note: The present sequence is not shown in the specification but  
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see  
 CC AAU00246)  
 XX  
 SQ Sequence 199 AA;  
 Query Match 100.0%; Score 89; DB 4; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RIMEKADSNKTRIDEANQ 18  
 DB 180 RIMEKADSNKTRIDEANQ 197  
 RESULT 11  
 AAU00264  
 ID AAU00264 standard; protein; 200 AA.  
 XX  
 AC AAU00264;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Synaptosomal-associated protein, SNAP25, mutant 1-200(R198T).  
 XX  
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KW synaptosomal-associated protein; mouse; mutant; mutein;  
 KW N-ethylmaleimide-sensitive fusion protein;  
 KW soluble NSF-attachment protein receptor.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 198  
 FT /note= "Wild-type Arg substituted by Thr"  
 XX  
 PN WO200118038-A2.

XX 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-GB003196.  
 XX  
 PR 20-AUG-1999; 99US-0149993P.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
 XX  
 DR WPI; 2001-226739/23.  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by a  
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
 PT resistant or toxin-inhibitory SNARE.  
 XX  
 PS Example 1; Page; 131pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant 1-200(R198T), used in a new method of  
 CC treating a patient suffering from poisoning or at risk of poisoning by a  
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-  
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the  
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating  
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a  
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
 CC or a recombinant polynucleotide encoding the SNARE is useful in the  
 CC manufacture of a medicament for the treatment of a patient suffering from  
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from  
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a  
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
 CC either of these SNARE polypeptides are useful in the manufacture of  
 CC medicament for the treatment of a patient in need of inhibition of SNARE-  
 CC dependent exocytosis from a cell capable of performing SNARE-dependent  
 CC exocytosis. The method of treatment is relatively fast, thus alleviating  
 CC the symptoms when most severe and taking the patient out of critical  
 CC state. Note: The present sequence is not shown in the specification but  
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see  
 CC AAU00246)  
 XX  
 SQ Sequence 200 AA;  
 Query Match 100.0%; Score 89; DB 4; Length 200;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RIMEKADSNKTRIDEANQ 18  
 DB 180 RIMEKADSNKTRIDEANQ 197  
 RESULT 12  
 AAU02637  
 ID AAU02637 standard; protein; 201 AA.  
 XX  
 AC AAU02637;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).  
 XX  
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KW synaptosomal-associated protein; mouse; mutant; mutein;  
 KW N-ethylmaleimide-sensitive fusion protein;  
 KW soluble NSF-attachment protein receptor.  
 XX  
 OS Mus sp.

OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 198  
FT /note= "Wild-type Arg substituted by Thr"  
XX  
XX  
PN WO200118038-A2.  
XX  
XX 15-MAR-2001.  
XX  
XX 18-AUG-2000; 2000WO-GB003196.  
PF  
XX 20-AUG-1999; 99US-0149993P.  
XX  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
PI  
XX WPI; 2001-226739/23.  
XX  
XX Treating a patient suffering from poisoning or at risk of poisoning by a  
PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
PT resistant or toxin-inhibitory SNARE.  
XX  
PS Example 1; Page; 131pp; English.  
XX  
XX The sequence represents the amino acid sequence of synaptosomal-  
CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of  
CC treating a patient suffering from poisoning or at risk of poisoning by a  
CC clostridial toxin, comprising supplying a SNARE (soluble (N-  
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
CC a cell of the patient, where the SNARE is resistant to proteolysis by the  
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating  
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
CC capable of performing SNARE-dependent exocytosis, comprises supplying a  
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
CC or a recombinant polynucleotide encoding the SNARE is useful in the  
CC manufacture of a medicament for the treatment of a patient suffering from  
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from  
CC botulism or tetanus. The fragment, variant, fusion or derivative of a  
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
CC either of these SNARE polypeptides are useful in the manufacture of  
CC medicament for the treatment of a patient in need of inhibition of SNARE-  
CC dependent exocytosis from a cell capable of performing SNARE-dependent  
CC exocytosis. The method of treatment is relatively fast, thus alleviating  
CC the symptoms when most severe and taking the patient out of critical  
CC state. Note: The present sequence is not shown in the specification but  
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see  
CC AAU00246)  
XX  
SQ Sequence 201 AA;  
  
Query Match 100.0%; Score 89; DB 4; Length 201;  
Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RIMEKADSNKTRIDEANQ 18  
Db |||||  
180 RIMEKADSNKTRIDEANQ 197  
  
RESULT 13  
AAU00265  
ID AAU00265 standard; protein; 202 AA.  
XX  
AC AAU00265;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Synaptosomal-associated protein, SNAP25, mutant 1-202(R198T).  
XX

KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
KW synaptosomal-associated protein; mouse; mutant; mutein;  
KW N-ethylmaleimide-sensitive fusion protein;  
KW soluble NSF-attachment protein receptor.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 198  
FT /note= "Wild-type Arg substituted by Thr"  
XX  
XX WO200118038-A2.  
PN  
XX 15-MAR-2001.  
PD  
XX 18-AUG-2000; 2000WO-GB003196.  
PF  
XX 20-AUG-1999; 99US-0149993P.  
PR  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
PI  
XX WPI; 2001-226739/23.  
DR  
XX  
XX Treating a patient suffering from poisoning or at risk of poisoning by a  
PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
PT resistant or toxin-inhibitory SNARE.  
XX  
PS Example 1; Page; 131pp; English.  
XX  
XX The sequence represents the amino acid sequence of synaptosomal-  
CC associated protein, SNAP25, mutant 1-202(R198T), used in a new method of  
CC treating a patient suffering from poisoning or at risk of poisoning by a  
CC clostridial toxin, comprising supplying a SNARE (soluble (N-  
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
CC a cell of the patient, where the SNARE is resistant to proteolysis by the  
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating  
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
CC capable of performing SNARE-dependent exocytosis, comprises supplying a  
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
CC or a recombinant polynucleotide encoding the SNARE is useful in the  
CC manufacture of a medicament for the treatment of a patient suffering from  
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from  
CC botulism or tetanus. The fragment, variant, fusion or derivative of a  
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
CC either of these SNARE polypeptides are useful in the manufacture of  
CC medicament for the treatment of a patient in need of inhibition of SNARE-  
CC dependent exocytosis from a cell capable of performing SNARE-dependent  
CC exocytosis. The method of treatment is relatively fast, thus alleviating  
CC the symptoms when most severe and taking the patient out of critical  
CC state. Note: The present sequence is not shown in the specification but  
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see  
CC AAU00246)  
XX  
SQ Sequence 202 AA;  
  
Query Match 100.0%; Score 89; DB 4; Length 202;  
Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RIMEKADSNKTRIDEANQ 18  
Db |||||  
180 RIMEKADSNKTRIDEANQ 197  
  
RESULT 14  
AAU02636  
ID AAU02636 standard; protein; 203 AA.

XX AC AAU02636;  
XX DT 12-SEP-2001 (first entry)  
XX DE Synaptosomal-associated protein, SNAP25, mutant 1-203 (R198T).  
XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
XX KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
XX KW synaptosomal-associated protein; mouse; mutant; mutein;  
XX KW N-ethylmaleimide-sensitive fusion protein;  
XX KW soluble NSF-attachment protein receptor.  
XX OS Mus sp.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"  
XX FT  
XX PN WO200118038-A2.  
XX PD 15-MAR-2001.  
XX PF 18-AUG-2000; 2000WO-GB003196.  
XX PR 20-AUG-1999; 99US-0149993P.  
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;  
XX DR WPI; 2001-226739/23.  
XX PT Treating a patient suffering from poisoning or at risk of poisoning by a  
XX PT clostridial toxin, e.g. botulism, comprises administering a toxin-  
XX PT resistant or toxin-inhibitory SNARE.  
XX PS Example 1; Page; 131pp; English.  
XX CC The sequence represents the amino acid sequence of synaptosomal-  
XX CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of  
XX CC treating a patient suffering from poisoning or at risk of poisoning by a  
XX CC clostridial toxin, comprising supplying a SNARE (soluble (N-  
XX CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to  
XX CC a cell of the patient, where the SNARE is resistant to proteolysis by the  
XX CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin  
XX CC (toxin-inhibitory SNARE). The protein can be used in a method of treating  
XX CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell  
XX CC capable of performing SNARE-dependent exocytosis, comprises supplying a  
XX CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE  
XX CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE  
XX CC or a recombinant polynucleotide encoding the SNARE is useful in the  
XX CC manufacture of a medicament for the treatment of a patient suffering from  
XX CC poisoning or at risk of poisoning by clostridial toxin, e.g. from  
XX CC botulism or tetanus. The fragment, variant, fusion or derivative of a  
XX CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
XX CC either of these SNARE polypeptides are useful in the manufacture of  
XX CC medicament for the treatment of a patient in need of inhibition of SNARE-  
XX CC dependent exocytosis from a cell capable of performing SNARE-dependent  
XX CC exocytosis. The method of treatment is relatively fast, thus alleviating  
XX CC the symptoms when most severe and taking the patient out of critical  
XX CC state. Note: The present sequence is not shown in the specification but  
XX CC is derived from the mouse SNAP-25 sequence given in figure 8 (see  
XX CC AAU00246)  
XX SQ Sequence 203 AA;  
XX CC Query Match 100.0%; Score 89; DB 4; Length 203;  
XX CC Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
XX CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18

Db 180 RIMEKADSNKTRIDEANQ 197  
RESULT 15  
AAW30103  
ID AAW30103 standard; peptide; 206 AA.  
XX AC AAW30103;  
XX DT 06-APR-1998 (first entry)  
XX DE Synaptosomal associated protein.  
XX KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;  
XX KW excitation-secretory uncoupling peptide; catecholamine secretion;  
XX KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
XX KW synaptosomal associated protein; SNAP-25.  
XX OS Homo sapiens.  
XX PN WO9734620-A1.  
XX PD 25-SEP-1997.  
XX PF 18-MAR-1997; 97WO-US004393.  
XX PR 18-MAR-1996; 96US-0013599P.  
XX PA (REGC ) UNIV CALIFORNIA.  
XX PI Montal M;  
XX DR WPI; 1997-479986/44.  
XX PT Excitation-secretory uncoupling peptide(s) for inhibiting  
XX PT neuro:transmitter release - used particularly for treating muscle  
XX PT spasticity, and for delivering drugs specifically to neural cells.  
XX PS Disclosure; Page 27-28; 61pp; English.  
XX CC This sequence represents the human 25 kD synaptosomal associated protein  
XX CC (SNAP-25), which is an inhibitory agent of the invention. The agents of  
XX CC the invention inhibit secretion of neurotransmitter from neuronal cells  
XX CC and is an excitation-secretory uncoupling peptide (I) of at least 20  
XX CC amino acids (aa) all of which correspond substantially to any one of  
XX CC AAW30097-W30102, or more generally any (I) that inhibits 50% of  
XX CC catecholamine secretion from bovine chromaffin cells at a concentration  
XX CC of 10 microM, especially 0.25 microM, or less. (I) are used, as a  
XX CC replacement for Clostridium toxin, to inhibit release of  
XX CC neurotransmitters from synaptic vesicles, specifically for reducing  
XX CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of  
XX CC intracellular distribution of (I). Compounds for delivering the drug to  
XX CC neural cells provide targeted drug delivery, e.g. of substance P to brain  
XX CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not  
XX CC toxic or immunogenic and are more readily available. Their therapeutic  
XX CC effect lasts for several days or weeks, so lower doses or less frequent  
XX CC treatments are required  
XX SQ Sequence 206 AA;  
XX CC Query Match 100.0%; Score 89; DB 2; Length 206;  
XX CC Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
XX CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18  
Db 180 RIMEKADSNKTRIDEANQ 197Search completed: March 9, 2004, 11:07:36  
Job time : 50.6216 secs